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4 US-09-328-35-4782 Sequence 4 US-09-902-540-11195 Sequence 4 US-09-543-681A-6790 Sequence 4 US-09-602-787A-282 Sequence	3 US-09-066-047-3 Sequence 4 US-09-252-9914A-18092 Sequence 3 US-09-380-420C-2 Semience	4 US-09-899-642A-2 Sequence	4 US-09-949-018-11/28 Sequence	4 US-09-543-681A-7562 Sequence 4 US-10-028-272-5 Sequence	4 US-09-949-016-6911 Sequence 6911	4 US-09-949-016-9814 Sequence 9814 4 US-09-949-016-6008 Sequence 6006	4 US-09-252-991A-31905 Sequence 3190	4 US-09-540-419C-23 Sequence 23,	4 US-09-252-991A-27902 Sequence 2790	4 US-09-902-540-12710 Sequence 12	4 US-09-352-9912-19581 Semience 19	4 US-10-028-272-3 Sequence 3,	4 US-10-028-272-2 Sequence 2, Appl	4 US-09-489-039A-7465 Sequence 7465, A	4 US-09-894-998A-26 Sequence 26, App	4 US-IU-Z3/-D5I-Z6 Sequence 3	4 US-09-252-991A-18711 Sequence	4 US-09-949-016-8473 Sequence	4 US-09-949-016-8474 Sequence	4 US-09-949-016-8475 Sequence	4 US-09-949-016-10692 Seguence (4 US-09-949-016-10693 Sequence	4 US-09-919-039-58 Sequence	4 US-09-949-016-11057 Sequence	4 US-09-949-016-11058 Sequence	4 US-09-949-016-11060 Sequence	4 US-09-949-016-8469 Sequence	4 US-09-949-016-8470 Sequence	4 US-09-949-016-84/1 Sequence 4 US-09-949-016-8472 Sequence	4 US-09-711-164-401 Sequence	3 US-09-207-857-2 Sequence	3 US-09-293-303-2 Sequence 4 US-09-909-280A-2 Semience	4 US-09-060-939A-2 Sequence	4 US-09-248-796A-19646 Sequence	4 US-08-857-636-60 Sequence	2 US-U8-540-406-10 Seguence 3 HS-08-656-055-10 Semience	3 US-08-954-668-10 Sequence	4 US-08-918-658-10 Sequence	4 US-09-724-631-10 Sequence	4 03-08-934-/01A-10 Sequence 10, 5 PCT-US95-13233-10	2 US-08-540-406-19 Sequence 19,	3 US-08-656-055-19 Sequence 19,	3 US-U8-954-668-19 Sequence 19,	4 US-08-288-140-3 Sequence 3, 4 US-08-918-658-19 Sequence 19.	4 US-09-724-631-19 Sequence 19,	4 US-08-954-701A-19 Seguence 19,	5 PCT-US95-13233-19 Sequence 19,	6 5206163-3 Patent No. 520 6 5206163-3	2 US-07-642-734C-5 Sequence 5. 2	3 US-08-439-009A-5 Sequence 5,	4 US-09-252-991A-31064 Sequence 31(
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Sequence 2, Application US/09671089;
Patent No. 6780846;
GENERAL INFORMATION;
APPLICANT: Q.Mahony, Daniel J.
APPLICANT: Q.Mahony, Daniel J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM;
FILE REFERENCE: E1067/2001B
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/156,246
PRIOR PILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
PEAT
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; OTHER INFORMATION: linked to FITC-LC
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US-09-671-089-3

| Sequence 3, Application US/09671089
| Sequence 3, Application US/09671089
| Patent No. 6780846
| GENERAL INFORMATION:
| APPLICANT: CAMBATION:
| APPLICANT: CAMBATION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
| TITLE OF INVESTION: MEMBREN US/09/671,089
| CURRENT APPLICATION NUMBER: US/09/671,089
| CURRENT FILING DATE: 1999-09-27
| PRIOR APPLICATION NUMBER: 60/156,246
| PRIOR FILING DATE: 1999-09-27
| NUMBER OF SEQ ID NOS: 59
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 3
| LENGTH: 16
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Query Match
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Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 15; Conservative 0; Mismatches 0;
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Sequence 48, Application US/09671089; Patent No. 6780846
GENERAL INFORMATION:
APPLICANT: O'MAHONY, Daniel J.
RAPLICANT: -LambKHH, Imelda J.
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Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
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PRIOR FILING DATE: 1999-09-27
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Patent No. 6780846

GENERAL INFORMATION

APPLICANT: Qualpory, Daniel J.

APPLICANT: Lambkin, Imelda J.

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

FILE REFERENCE: E1067-20018

CURRENT APPLICATION NUMBER: US/09/671,089

CURRENT APPLICATION NUMBER: 60/156,246

PRIOR APPLICATION UNMER: 60/156,246

PRIOR PLING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin version 3.1

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APPLICANT: O'MADON, Daniel J.
APPLICANT: Cambrin, Imelda J.
APPLICANT: Lambrin, Imelda J.
TITLE OP INVENTION: MABRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE REFERENCE: E1067/20018
CURRENT APPLICATION NUMBER: US/09/671,089
PRIOR APPLICATION NUMBER: 60/156,246
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE REFERENCE: E1067/20018
CURRENT APPLICATION NUMBER: US/09/671,089
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 6/156,246
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
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LENGTH: 16
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                                                                                                                                                                                                                                                                     OTHER INFORMATION: dansylated membrane translocating peptide
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 68; DB 4; Length 16; 100.0%; Pred. No. 6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Pred. No. 7.2e-05;
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US-09-671-089-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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US-09-671-089-5
'Sequence 5, Application US/09671089
'Patent No. 6780846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
                                                                                                                                                                                                                                                                                                               NAME/KEY: MOD_RES
LOCATION: (1)...(1)
COTHER INFORMATION: dansylated
US-09-671-089-48
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 15; Conservative
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Patent No. 624658

GENERAL INFORMATION:
APPLICANT: Lona with P.
APPLICANT: Rojas, Mauricio
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of PITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
FILE REFERENCE: VU9941
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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OTHER INFORMATION: Description of Artificial Sequence: Am:
OTHER INFORMATION: sequence of peptide which transports pro
OTHER INFORMATION: through the cell membrane into the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.4%; Score 54; DB 3; Length 12; Best Local Similarity 100.0%; Pred. No. 0.0089; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         Length 16;
                                                                                                                                                                           ; OTHER INFORMATION: membrane translocating peptide, cyclic US-09-671-089-5
                                                                                                                                                                                                                                                    Query Match
94.1%; Score 64; DB 4; I
Best Local Similarity 93.3%; Pred. No. 0.00027;
Matches 14; Conservative 0; Mismatches 1;
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CURRENT FILING DATE: 1998-11-04
EARLIER APPLICATION NUMBER: 60/080,083
EARLIER FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
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US-09-562-868-1
; Sequence 1, Application US/09562868
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.1
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ORGANISM: Artificial Sequence
                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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NAME/KEY: PEPTIDE
LOCATION: (1)..(12)
PUBLICATION INFORMATION:
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PAGES: 370-375
DATE: 1998-04-01
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Sequence 8, Application US/10083889

Patent No. 6673894

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
FILE REFERENCE: 16850-7331
CURRENT FELING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/271,798
PRIOR FILING DATE: 2001-02-27
RUGHER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Word 97
SEQ ID NO 8
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Sequence 1, Application US/10116288A.

Patent No. 6780843.

GENERAL INFORMATION:

APPLICANT: Lin, Yao-Zhong

APPLICANT: Lin, Yao-Zhong

APPLICANT: Tonahue, John P.

APPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of PAPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of Patent No. 6780843.

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of PAPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of Patent No. 6780843.

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of PAPLICANTON NUMBER: 09/562,868

PRIOR FILING DATE: 2000-05-01

PRIOR FILING DATE: 1998-11-04

PRIOR FILING DATE: 1998-11-04

PRIOR FILING DATE: 1998-03-31

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

TENGTH: 170
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LOCATION: (1)..(12)
PUBLICATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 12; Conservative
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                                          1 AAVLLPVLLAAP 12
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US-10-083-889-8
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US-10-083-889-8
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Patent No. 6673574

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mehta, William
APPLICANT: Ret, Martha V.L.
ITILE OF INVENTION: INPROVED ORAL DELIVERY OF PEPTIDES USING ENZYME-CLEAVABLE MEMBRAN
TITLE OF INVENTION: TRANSLOCATORS
FILE REFERENCE: P/546-247
CURRENT APPLICATION NUMBER: US/09/997,465B
CURRENT APPLICATION DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
                                     APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
FILE REFERENCE: 22000.0037u2
CURRENT PRILICATION NUMBER: US/09/562,868
CURRENT PILLING DATE: 2000-05-01
PRIOR FILLING DATE: 2000-05-01
PRIOR FILLING DATE: 1998-03-31
PRIOR FILLING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 12
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NAME/KSY: PEPTIDE
LOCATION: (1)...(12)
PUBLICATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
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100.0%; Pred. No. 0.0089;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
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LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Rojas, Mauricio
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
FILE REFERENCE: 22000.009703
FILE REFERENCE: 22000.009703
FILE PAPLICATION NUMBER: 09/562,868
FRIOR APPLICATION NUMBER: 09/562,868
FRIOR APPLICATION NUMBER: 09/186,170
FRIOR APPLICATION NUMBER: 09/186,170
FRIOR APPLICATION NUMBER: 60/080,083
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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Genesiuttle Biopharm, Inc.

APPLICANT: Hwu, Paul L.

TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
FILE REFERENCE: MEHB 02-340

CURRENT APPLICATION NUMBER: US/10/144,549

CURRENT FILING DATE: 2002-05-13

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1

SEQ ID NO 19

LENGTH: 12
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OTHER INFORMATION: Kaposi FGF signal sequence.
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ORGANISM: Artificial Sequence
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Best Local Similarity
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APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imelda J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE REFERENCE: E1067/20018
CURRENT FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: O'MAHONY, Daniel J.

APPLICANT: Lambkin, Imelda J.

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20018

CURRENT APPLICATION NUMBER: US/09/671,089

CURRENT FILING DATE: 2000-9-27

PRIOR APPLICATION NUMBER: 60/156,246

PRIOR FILING DATE: 1999-09-27
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                                                                                                                                                                      DB 4; Length 12; 0.0089;
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                                                                                                                                                                                                                                0; Indels
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US-09-671-089-14
                                                                                                                                                                   ch 79.4%; Score 54; DB 1 Similarity 100.0%; Pred. No. 0.0 12; Conservative 0; Mismatches
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Patent No. 6780846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09671089 Patent No. 6780846
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 12; Conservative
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Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
                           ; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-10-116-288A-1
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US-09-671-089-14
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US-09-671-089-1
VOLUME: 16
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Sequence 24, Application US/09671089
; Sequence 24, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT O'Mahony, Daniel J.
; APPLICANT O'Mahony, Daniel J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; TITLE OF INVENTION NUMBER: US/09/671,089
; CURRENT APPLICANTON NUMBER: US/09/671,089
; CURRENT PELLING DATE: 2000-09-27
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 24
; LENGTH: 17
                                                                                                                                                                                                         RESULT 17
US-09-671-089-58

1 Sequence 58, Application US/09671089

2 Fatent No. 678046

3 GENERAL INFORMATION:

APPLICANT: O'MAHONY, Daniel J.

APPLICANT: Lambkin, Imelad J.

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE OF INVENTION NUMBER: US/09/671,089

CURRENT APPLICATION NUMBER: US/09/671,089

CURRENT PILING DATE: 2000-09-27

PRIOR PILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 59

SOCTWARE: Patentin version 3.1

EENGTH: 14
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; OTHER INFORMATION: membrane translocating peptide, cyclic internal
US-09-671-089-58
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Pred. No. 0.04;
0; Mismatches 1; Indels
Indels
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Pred. No. 0.015;
Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 92.3%;
                                                                                           1 KKAAAVLLPVLLA 13
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Best Local Similarity 92.3
Matches 12, Conservative
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12; Conservative
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US-09-186-170-9
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                                                                                                                                                                                                                                                                              | Fatent No. 6780843|
| GENERAL INFORMATION: APPLICANT: Lin, Yao-Zhong | APPLICANT: Lin, Yao-Zhong | APPLICANT: Lin, Yao-Zhong | APPLICANT: Lin, Yao-Zhong | APPLICANT: Tan, Zhongjia | TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of FATILE OF INVENTION: "Sequence and Method for Genetic Engineering of TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity" | FILE REFERENCE: 22000.059703 | CURRENT FILING DATE: 2000-05-01 | PRIOR PILING DATE: 2000-05-01 | PRIOR FILING DATE: 1998-11-04 | PRIOR FILING DATE: 1998-11-04 | PRIOR FILING DATE: 1998-13-31 | NUMBER OF SEQ ID NOS: 23 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NO 20 | SEQ I
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APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Inelda J.
TITLE OF INFORMATION:
FILE REFERENCE: E1067/20018
FILE REPERENCE: E2067/20018
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: G6/156,246
PRIOR FILING DATE: 1999-09-27
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; OTHER INFORMATION: membrane translocating peptide, cyclic internal

US-09-671-089-7
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Pred. No. 0.015;
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; Sequence 20, Application US/10116288A
; Patent No. 6780843
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92.3%;
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SOFWARE: Patentin version 3.1
SEQ ID NO 7
EMOCH: 14
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
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Sequence 9. Application US/09562868

Sequence 9. Application US/09562868

GENERAL INFORMATION:

APPLICANT: Lin, Yao-Zhong

APPLICANT: Lonahue, John P.

APPLICANT: Tan, Zhongjian

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

CURRENT APPLICATION NUMBER: 00/096.083

PRIOR APPLICATION NUMBER: 00/080,083

PRIOR APPLICATION NUMBER: 09/186,170

PRIOR APPLICATION NUMBER: 09/186,170
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                 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Danahue, John P.

APPLICANT: Donahue, John P.

APPLICANT: Rojas, Mauricio

APPLICANT: Rojas, Mauricio

APPLICANT: Rojas, Mauricio

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity:

PILE REFERENCE: VU9841

CURRENT APPLICATION NUMBER: US/09/186,170

CURRENT FILING DATE: 1998-11-04

EARLIER PILING DATE: 1998-11-04

NUMBER OF SEQ ID NOS: 18

SOFTHARE: PATENTIN VOS: 18

SOFTHARE: PATENTIN VOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of peptide which transports proteins OTHER INFORMATION: through the cell membrane into the cell. FEATURE: FEATURE: NAME/KEY: PEFTIDE LOCATION: (1)...(11) PUBLICATION: (1)...(11) FUBLICATION INFORMATION: TITLE: "Genetic Engineering of Proteins with Cell Membrane TITLE: Permeability"
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0, Indels
Sequence 9, Application US/09186170
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ORGANISM: Artificial Seguence
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ORGANISM: Artificial Sequence
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ISSUE: April
PAGES: 370-375
DATE: 1998-04-01:
RELEVANT RESIDUES: 1 TO 12
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 11
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Matches 11; Conservative
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LENGTH: 11
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Sequence 9, Application US/10116288A

Sequence 9, Application US/10116288A

Sequence 9, Application US/10116288A

GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Donahue, John P.
APPLICANT: Donahue, John P.
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
FILE REFERENCE: 22000.0097104

FILE REFERENCE: 22000.0097104

FILE REFERENCE: 22000.0097104

FRIOR PLING DATE: 2002-04-04

FRIOR PLING DATE: 1998-11-04

FRIOR FILING DATE: 1998-03-31

NUMBER OF SEQ ID NOS: 23

SEQ ID NO 9

LENGTH: 11

TWOE: DON

LENGTH: 11

TWOE: DON

LENGTH: 11

TWOE: DON

LENGTH: 11

TWOE: DON
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence of peptide which transports proteins
OTHER INFORMATION: through the cell membrane into the cell.
NAME/KEY: PERTIDE
I.OCATION: (1)...(1)
PUBLICATION INFORMATION:
AUTHORS: Rojas, M. et al.
ITLE: Genetic Engineering of Proteins with Cell Membrane
IIILE: Permeability"
ITLE: Permeability"
INCURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
US-09-562-868-9
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LOCATION: (1)..(11)
PUBLICATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
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Pred. No. 0.037;
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VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
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Best Local Similarity
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                                                                                                                                                                    Sequence 19, Application US/09671089
; Sequence 10, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
   APPLICANT: O'MAHONY, Daniel J.
   TITLE OF INVENTION: MEMBRRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT APPLICATION NUMBER: 60/156,246
; PRIOR APPLICATION NUMBER: 60/156,246
; RIOR PILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
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Fatent No. 6780846

GENERAL INFORMATION;

APPLICANT: CAMBORN, Daniel J.

APPLICANT: Lambkin, Imelda J.

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE REFERENCE: E1067/20018

CURRENT APPLICATION NUMBER: US/09/671,089

CURRENT FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin version 3.1

SSOTHARE: Patentin version 3.1

LENGTH: 13
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  Indels
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// OTHER INFORMATION: membrane translocating peptide
US-09-671-089-19
  0; Mismatches
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  11; Conservative
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US-09-671-089-19
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US-09-671-089-10
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RESULT 24 US-09-186-170-5

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| Sequence 5, Agelsteaton US/09186170
| Sequence 5, Agelsteaton US/09186170
| Patent No. 6248558
| APPLICANT: DAMARY 10.00
| APPLICANT 10.00
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US-09-671-089-15

US-09-671-089-15

Sequence 15, Application US/09671089

Patent No. 6780846

GENERAL INFORMATION:
APPLICAMT: O'MAHONY, Daniel J.
APPLICAMT: Lambkin, Imelda J.
TITLE OF INVERTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20018
CURRENT APPLICATION NUMBER: US/09/671,089
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/156,246
PRIOR PILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 15
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Indels
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Best Local Similarity 91.7%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches
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100.0%; Pred. No. 0.12;
tive 0; Mismatches
Mismatches
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Best Local Similarity 100.
Matches 11; Conservative
11; Conservative
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                                                    4 AAVLLPVLLAA 14
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US-09-671-089-59
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Matches
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GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
FILE REFERENCE: 22000.0097103
FILE REFERENCE: 22000.0097103
CURRENT FILING DATE: 2002-04-04
FRIOR APPLICATION NUMBER: 09/186,170
FRIOR FILING DATE: 1998-11-04
FRIOR FILING DATE: 1998-11-04
FRIOR FILING DATE: 1998-11-04
FRIOR APPLICATION NUMBER: 09/186,170
FRIOR APPLICATION
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                OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of peptide which transports proteins OTHER INFORMATION: through the cell membrane into the cell.

NAME/KEY: PEPTIDE
LOCATION: (1)...(11)
PUBLICATION INFORMATION:
AUTHORS: ROJAS, M. et al.
TITLE: Permeability"
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PUBLICATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
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0.12;
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Pred. No.
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VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
US-09-562-868-5
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ORGANISM: Artificial Sequence
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VOLUME: 16
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Best Local Similarity
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Best Local Similarity
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NAME/KEY: PEPTIDE
LOCATION: (1)..(1
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PAGES: 370-375
DATE: 1998-04-01
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US-10-116-288A-5
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, OTHER INFORMATION: membrane translocating peptide US-09-671-089-23
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                                                                                                                                                                                                                                                                                                  Query Match 69.1%; Score 47; DB 4; Best Local Similarity 100.0%; Pred. No. 0.18; Matches 11; Conservative 0; Mismatches
            PRIOR APPLICATION NUMBER: 60/156,246
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
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NAME/KEY: PEPTIDE
LOCATION: (1)..(10)
PUBLICATION INFORMATION:
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PAGES: 370-375
DATE: 1998-04-01
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US-09-562-868-8
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; Sequence 59, Application US/09671089; Patent No. 6780846; GENERAL INFORMATION; PAPLICANT: O'MAHONY, Daniel J.
APPLICANT: Lambkin, Imelda J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE REFERENCE: E1067/20018
CURRENT APPLICATION NUMBER: US/09/671,089
CURRENT FILING DATE: 2000-09-27
PRIOR PILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
SEQ ID NO 59
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Sequence 6, Application US/09671089
Sequence 6, Application US/09671089
Sequence 6, Application US/09671089
GENERAL INFORMATION:
APPLICANT: Lambkin, Imelda J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REPERENCE: E1067/2010 1
CURRENT APPLICATION NUMBER: US/09/671,089
CURRENT FILING DATE: 1999-0-27
PRIOR APPLICATION NUMBER: 60/156,246
PRIOR APPLICATION UNDER: 60/156,246
PRIOR PILING DATE: 1999-0-27
NUMBER OF SEQ ID NOS: 59
SSOFTWARE: Patentin version 3.1
SSOFTMARE: Patentin version 3.1
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Patent No. 6780846
Patent No. 6780846
RABELICANTION:
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE REFERENCE: E1067/20018
CURRENT APPLICATION NUMBER: US/09/671,089
CURRENT FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.1%; Score 47; DB 4; Length 12; Best Local Similarity 91.7%; Pred. No. 0.13; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: membrane translocating peptide, cyclic US-09-671-089-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: membrane translocating peptide
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Sequence 8, Application US/09186170
Sequence 8, Application:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Rojas, Mauricon
APPLICANT: Rojas, Mauricon
APPLICANT: Rojas, Mauricon
APPLICANT: Pan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6248588
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6248588
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6248588
TITLE OF INVENTION NUMBER: US/09/186,170
CURRENT APPLICATION NUMBER: US/09/083
EARLIER PILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 8
LEMOTH: 10
                                                          Gaps
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Length 17;
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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PAGES: 370-375
DATE: 1998-04-01
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                                     APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Rojas, Mauricio
APPLICANT: Rojas, Mauricio
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
TITLE OF INVENTION: Processing with Cell Membrane Translocating Activity"
FILE REFERENCE: 2000-009705
CURRENT APPLICATION NUMBER: US/09/562,868
FRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 09/186,170
FRIOR APPLICATION NUMBER: 09/186,170
FRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 8
TENTING PATENTIAL NOS: 18
TENTING PATENTIAL NOS: 18
TENTING PATENTIAL NOS: 18
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Patent No. 6780843

GENERAL INPORANTION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lan, Zhongjia
APPLICANT: Rojas, Mauricio
APPLICANT: Pan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6780843
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6780843
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
PRIOR PLING DATE: 2000-009703
CURRENT FILING DATE: 2000-04-04
PRIOR PILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 23
SOFFWARE: Patentin Ver. 2.0
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OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence of peptide which transports proteins
OTHER INFORMATION: through the cell membrane into the cell.
NAME/KEY: PEPTIDE
LOCATION: (1)...(10)
PUBLICATION INFORMATION:
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TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
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Sequence 8, Application US/09562868
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
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US-09-186-170-4
; Sequence 4, Application US/09186170
; Sequence 4, Application US/09186170
; Sequence 4, Application US/09186170
; Patcett No. 624858
; APPLICANT: Lin, Yao-Zhong
; APPLICANT: Rojas, Mauricio
; APPLICANT: Rojas, Mauricio
; APPLICANT: Tan, Zhongjia
; TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
; Patent No. 624858
; TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
; FILE REFERENCE: VU9841
; CURRENT FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/080,083
; BARLIER FILING DATE: 1998-33-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 10
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NAME/KEY: PEPTIDE
LOCATION: (1)..(10)
PUBLICATION INFORMATION:
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.2%; Score 43; DB 3; Length 10;
100.0%; Pred. No. 0.47;
iive 0; Mismatches 0; Indels
                                                                                                                                                                              , OTHER INFORMATION: membrane translocating peptide, cyclic US-09-671-089-11
                                                                                                                                                                                                                                                                                                           0; Indels
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PRIOR APPLICATION NUMBER: 60/156,246
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
LENGTH: 12
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                                                                                                                                                     ORGANISM: Artificial Sequence
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PAGES: 370-375
DATE: 1998-04-01
RELEVANT RESIDUES: 1 TO 12
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Matches 10; Conservative
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RESULT 38 US-09-562-868-4

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| Sequence 4, Application Us/03562868 |
| PREARL NFORMATION: ASJ280 |
| APRILONI: ROBARTION: ADMANGED |
| APPLICANT: Roll NAVIATION: Sequence and Wethod for Genetic Engineering of PREARL NFORMATION: ADMANGED |
| APPLICANT: Roll NAVIATION: Sequence and Wethod for Genetic Engineering of PREARL STATION OF SEQUENCE WITH Call Membrane Translocating Activity* |
| TITLE OF INVARIANT ON PROPERTY OF SEQUENCE AND ACTIVITY* |
| TITLE OF INVARIANT ON PROPERTY OF SEQUENCE AND ACTIVITY* |
| TITLE OF INVARIANT ON PROPERTY OF SEQUENCE AND ACTIVITY* |
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Sequence 7, Application US/09562868

Sequence 7, Application US/09562868

Patent No. 6432680

GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Rojas, Mauricio
APPLICANTION: Sequence and Method for Genetic Engineering of
FILER PEFERRENCE: 2000-0097U2
CURRENT APPLICATION NUMBER: US/09/562,868
CURRENT FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
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                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence ORGANISM: Artificial Sequence: Amino acid OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of peptide which transports proteins OTHER INFORMATION: through the cell membrane into the cell.
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                                                                                                                                                                                                                                                                                                                                              NAME/KEY: PEPTIDE
LOCATION: (1)..(9)
PUBLICANO INPOGNATION:
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
VOUNAL: Nature Biotechnology
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TITLE: Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
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Pred. No. 4.1e+05;
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CURRENT FILING DATE: 1998-11-04
EARLIER APPLICATION WUNBER: 60/080,083
EARLIER FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 9
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ORGANISM: Artificial Sequence
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PAGES: 370-375
DATE: 1998-04-01
RELEVANT RESIDUES: 1 TO 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 9
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APPLICANT: GARY BRETON
TITLE OF INVENTION: ULCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: ULCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US 69/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 80-48
LENGTH: 191
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Parent No. 624858

GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Applas, Mauricto
APPLICANT: Applas, Mauricto
APPLICANT: Tan, Zhongia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Parent No. 624858
TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
FILE REFERENCE: VUS941
CURRENT APPLICATION NUMBER: US/09/186,170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of peptide which transports proteins OTHER INFORMATION: through the cell membrane into the cell.
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                                                                                                                                                                     FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(10)
PUBLICATION INFORMATION:
AUTHORS: Rojae, M. et al.
ATTILE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.2%; Score 43; DB 4; Length 10; 100.0%; Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8048, Application US/09543681A Patent No. 6605709
                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                           JOURNAL: Nature Biotechnology
VOLUWE: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 72.7
Matches 8, Conservative
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Matches 10; Conserv
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US-09-543-681A-8048
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US-09-186-170-7
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RESULT 46
US-09-252-991A-18288
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| GENERAL INFORMATION:
| APPLICANT: Lin, Yao-Zhong
| APPLICANT: Lin, Yao-Zhong
| APPLICANT: Donahue, John P.
| APPLICANT: Rojas, Mauricto
| TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
| TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
| TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
| TITLE OF INVENTION: UNMBER: 09/146
| PRIOR APPLICATION NUMBER: 09/562,868
| PRIOR FILING DATE: 1998-11-04
| PRIOR FILING DATE: 1998-11-04
| PRIOR FILING DATE: 1998-11-04
| PRIOR FILING DATE: 1998-03-31
| NUMBER OF SEQ ID NOS: 23
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 7
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                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of peptide which transports proteins OTHER INFORMATION: through the cell membrane into the cell.
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TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.8%; Score 42; DB 4; Length 9; 100.0%; Pred. No. 4.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                             0; Indels
                                                                                                      DB 4; Length 9;
                                                                                                                            4.1e+05;
                                                                                                  61.8%; Score 42; DB 100.0%; Pred. No. 4.1 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10116288A Patent No. 6780843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-671-089-21; Sequence 21, Application US/09671089; Patent No. 6780846; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
                                                                                                                                             9; Conservative
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LOCATION: (1)..(9)
PUBLICATION INFORMATION:
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                                                                                                    Query Match
Best Local Similarity
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; PAGES: 370-375
; DATE: 1998-04-01
US-10-116-288A-7
; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-09-562-868-7
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US-10-116-288A-7
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Sequence 18288, Application US/09252991A

Sequence 18288, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: US 60/094,190
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APPLICANT: O'Mahony, Daniel J.

APPLICANT: O'Mahony, Daniel J.

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE POF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE REPERENCE: E1067/20018

CURRENT APPLICATION NUMBER: US/09/671,089

CURRENT PILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/156,246

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin version 3.1

SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: O'MADONY, Daniel J.
APPLICANT: O'MADONY, Daniel J.
APPLICANT: Lambkin, Imelda J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE REFERENCE: E1067/20018
CURRENT APPLICATION NUMBER: US/09/671,089
CURRENT FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-27
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100.0%; Pred. No. 0.76;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.8%; Score 42; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 4.18+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: membrane translocating peptide, cyclic
US-09-671-089-12
                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: membrane translocating peptide US-09-671-089-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09671089 Patent No. 6780846
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SOFWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 11
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100...
Best Local 9; Conservative
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7 AAAVVLPVLL 16
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| Sequence 7, Application US/09689730
| Patent No. 6625024
| GENERAL INFORMATION:
| APPLICANT: SEIKI, Motcharu
| APPLICANT: SAIC, Hirosh
| APPLICANT: SHOW, Hirosh
| APPLICANT: SHOW, Hirosh
| TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
| FILE REPERENCE: 55.20P
| FILE REPERENCE: 55.20P
| CURRENT PILING DATE: 2000-10-13
| PRIOR PLILING DATE: 1995-06-07
| NUMBER OF SEQ ID NOS: 19
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SEXII, Motoharu
APPLICANT: SEXII, Motoharu
APPLICANT: SEXII, Motoharu
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-209
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO?
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                                                                                                                                                            Score 41; DB 4; Length 578;
Pred. No. 68;
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Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.8%; Score 40; DB 4; Length 30; 90.0%; Pred. No. 4.6; 1; Mismatches 0; Indels
                                                                                                                                                                                                 2; Indels
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Patent No. 6184022
                                                                                  ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.8%;
           1998-07-27
                                                                                                                                                          Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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182 RRSLAVLLPILLLA 195
PRIOR FILING DATE: 1998-07-;
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18288
LENGTH: 578
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9, Conservative
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7 AAAVVLPVLL 16
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ORGANISM: Homo sapiens
US-08-448-489-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-689-730-7
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Sequence 20502. Application US/09252991A

Sequence 20502. Application US/09252991A

Parent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ASSUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASSUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASSUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1990-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20502
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                                                         GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myacoccus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10 (15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12703
LENGTH: 263
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Pred. No. 44;
1; Mismatches 1; Indels
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US-09-902-540-12703
; Sequence 12703, Application US/09902540
; Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: June 2, 2005, 01:40:38
Job time : 34.125 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.8%;
                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Myxococcus xanthus US-09-902-540-12703
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Best Local Similarity 60.00
Best Local 9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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B8118 S33948 E7254 T3075 D859 JQ22 JQ22 A333 T020 S376	S599 A726 D022 D022 B843 B843 AB19 AC18 S129 S129 S425 B842	S113 B810 B820 H711 T508 H711 H877 T307 T307 T346	8008 PR0131 PR0131 PA123 PA1123 PA1123 PA1123 PA1123 PA1123 PA1123 PA1123 PA1123 PA1123 PA1123 PA1123 PA1123 PA1123	2 7.55501 2 7.75501 2 7.71839 2 7.74507 2 87.5419 2 86.9750 2 86.9750 2 86.9750 2 76.001 2 76.001 2 76.001 2 76.001 2 76.001 2 76.001 2 76.001 2 76.001 2 76.001 2 76.001
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ALIGNMENTS

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C;Accession: AF2275
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, B.; Bizer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitem. A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                A, Accession: AF2275
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-297 «KIR»
A, Residues: 1-297 «KIR»
A, Experimental gource: strain 16M
A, Experimental gource: strain 16M
A, Genetics:
A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A
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hypothetical protein F24J7.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 09-Jul-2004
C;Accession: T05209
R;Bevan, M.; Vitale, D.; Liguori, R.; Argiriou, A.; De Simone, V.; Bancroft, I.; Mewes, submitted to the Protein Sequence Database, February 1998
A;Reference number: 215403
A;Reference T05209
A;Molecule type: DNA
A;Residues: 1-939 cBSV.
A;Cross-references: UNIPROT: O49467; EMBL: AL021768; GSPDB: GN00062; AISP: F24J7.50
A;Experimental source: cultivar Columbia; BAC clone F24J7
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A;Status: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9Y8Y4; DDBJ:AP000064; NID:g5105945; PIDN:BAA81516.1; PID:d1
A;Experimental source: strain X1
A;Gene: APE2500
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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Pred. No. 16;
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69.2%; Pred. No. 45;
tive 2; Mismatches 2; Indels
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Matches 9; Conservative
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160 AAALLIPVLLA 170
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A,Gene: ATSP:F24J7.50
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RESULT 1 AF3275 transporter, dme family BMEI0187 [imported] - Brucella melitensis (strain 16M) , C;Species: Brucella melitensis us-10-764-235-2.rpr

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C;Accession: A97600
R;Goodher, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., Science 294, 2323-2328, 2001
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q8UDX0; GB:AE007869; PIDN:AAK87754.1; PID:g15157122; GSPDB:C
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A;Bxperimental source: strain X1
C;Genetics:
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. (Silvod, D.W.; Setubal, J.C.; Kaul, R.; Monthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell stage, B.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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C,Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A72698
30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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Pred. No. 43;
1; Mismatches
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Pred. No. 19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: AGR C 3631
A,Map position: circular chromosome
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Best Local Similarity 75.0%;
Matches 9; Conservative
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180 AAKLLPLLAAAP 191
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-163 <KUR>
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A;Molecule type: DNA
A;Residues: 1-390 <KAW>
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A; Residues: 1-431 < KUR:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conserved hypothetical protein Atu1998 [imported] - Agrobacterium tumefaciens (strain CS C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Accession: A12821
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R; Wood, D.W.; Setubal, Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                    lipid transfer protein - spinach
(Species: Spinacia oleracea (spinach)
(Species: Spinacia oleracea (spinach)
(Species: Jabu-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
(Space: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
(Spacession: T09155
(R) Bernhard, W.R.; Thoma, S.; Botella, J.; Somerville, C.R.
(R) Brant Physiol. 95, 164-170, 1991
(R) A.Fitle: Isolation of a cDNA clone for spinach lipid transfer protein and evidence that A; Reference number: Z16594
(R) A.Fatulus: preliminary; translated from GB/EMBL/DDBJ
(R) A.Fatulus: preliminary; translated from GB/EMBL/DDBJ
(R) A.Fatulus: 1-117 ebb.
(Species - 1-117 ebb.)
(Spe
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A;Experimental source: strain C58 (Dupont)
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C;Species: Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8. A;Reference number: AB2577; MUID:21608550; PMID:11743193
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                                   Score 41; DB 2; Length 1172;
Pred. No. 81;
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                                                                                                   2; Mismatches
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                                Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
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Best Local Similarity
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A;Residues: 1-158 <KUR>
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$Species: Homo sapiens (man)
$Date: 17-May-1996 #sequence revision 17-May-1996 #text change 09-Jul-2004
$Date: 17-May-1996 #sequence revision 17-May-1996 #text change 09-Jul-2004
$Accession: 138028; G02274; T38046; S78011; S45341; S71384

ur. J. Biochem. 231, 602-608, 1995

"Title: CDNA sequence and mRNA tissue distribution of a novel human matrix metalloprot: Reference number: 138028; WUID:95377289; PMID:7649159

*Accession: 138028
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A;Accession: G02274
A;Accession: G02274
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Graus: preliminary; translated from GB/EMBL/DDBJ
A;Crose-references: EMBL:U41078; NID:g1127836; PIDN:AAA83770.1; PID:g1127837
A;Crose-references: EMBL:U41078; NID:g1127836; PIDN:AAA83770.1; PID:g1127837
B;Okada, A; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, EProc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal c: A;Accession: 138046; MID:7708715
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C; Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote C; Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote C; Superfamily: interstitial collagenase; hemopexin repeat C; Reywords: glycoprotein); hydrolase; metalloprotein signal sequence #status predicted <SIG.
F; 24-97/Domain: signal sequence #status predicted <PRO>
F; 24-97/Domain: matrix metalloproteinase homology <WMP>
F; 98-582/Product: matrix metalloproteinase homology <WMP>
F; 285-313/Domain: hinge #status predicted <NAT>
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A;Cross-references: UNIPROT:P50281; EMBL:Z48481; NID:g963053; PIDN:CAA88372.1; PID:g9630
                                                                                                                                                                                                                                    matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human
N;Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteina
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A,Molecule type: mRNA
A,Residues: 1-7, 'S', 9-188 'K',190,'A',192-267,'K',269-272,'HY',275,'P',277-285,'KQ',288,
A,Cross-references: EMBL:D26512
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A;Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
A;Reference number: S71384; MUID:96397540; PMID:8804434
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A;Residues: 1-7,'S',9-337,'K',339-582 <SEI>
A;Cross-references: EMBL:D26512; NID:g793762; PIDN:BAA05519.1; PID:g793763
A;Sto, H.; Takino, T.; Okada, Y.; Cao, J.; Shinagawa, A.; Yamamoto, E.; Seiki, M.
Nature 370, 61-65, 1994
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A;Residues: 1-7,'S',9-582 <OKA>
A;Cross-references: EMBL:X83535; NID:g804993; PIDN:CAA58519.1; PID:g804994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Reference number: $78011
A;Accession: S78011
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A; Gene: GDB: MMP14; MT1-MMP
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A; Residues: 112-116 <SAW>
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R; Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F.
Proc. Natl. Acad. Sci. US.A. 92, 2730-2734, 1995
A; Accession: 148673
A; MUID: 95224014; PMID: 7708715
A; Accession: 148673
A; Molecule type: mRNA
A; Rasidues: preliminary; translated from GB/EMBL/DDBJ
A; Cross-references: EMBL: X83536; NID: 9804999; FIDN: CAA58520.1; PID: 9805000
C; Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein c; Superfamily: signal sequence #status predicted <SIG>F: 1-23/Domain: activation peptide #status predicted <PRO>F: 284/Domain: matrix metalloproteinase homology <WNP>
F: 61-284/Domain: matrix metalloproteinase homology <WNP>
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RiGoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUD:21608551; PMID:11743194

A; Reference B974, 2323-2328, 2001

A; Reference number: A97359; MUD:21608551; PMID:11743194

A; Rescidues: Dramary

A; Rossiques: 1-435 «KUR»

A; Rescidues: 1-435 «KUR»

A; Cross-references: UNIPROT:Q8UI19; GB:AE007869; PIDN:AAK86294.1; PID:g15155408; GSPDB:G

A; Genetics:
A; And position: circular chromosome
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F;393,239,243,249/Binding afte: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;229,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F;240/Active site: Glu #status predicted
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C;Species: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Agrobacterium tumefaciens
Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                    Pred. No. 47;
1; Mismatches
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                                                                                                                                                                                                   Score 40;
Pred. No.
    source: strain C58 (Dupont)
    A;Experimental source: strain C58 (I
C;Genetics:
A;Gene: excQ
A;Gene: excQ
A;Map position: circular chromosome
                                                                                                                                                                                               Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
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227 KTAAMLLPVTLA 238
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231 KTAAMLLPVTLA 242
                                                                                                                                                                                                                                                                                                                                                          2 KAAAVLLPVLLA 13
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A; Accession: A33322
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           C, Genetics:
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Nyletranae names: membrane-type metalloproteinase
C;Special Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 184471; 151946
C;Accession: 184471; 151946
R;Okada, A.; Bellocg, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F.
R;Okada, A.; Bellocg, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F.
R;Okada, A.; Bellocg, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F.
R;Okada, A.; Bellocg, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F.
R;Okada, A.; Bellocg, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F.
A;Ttle: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal ce
A;Rescasion: 18441
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 11592 eRB.
A;Accession: 161946
A;
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By Pothetical protein MYPU_1970 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

Cispecies Mycoplasma pulmonis

Cispecies Res 29, 2145-2153, 2001

A; Reference mumber: A9512; MUD:21267165; PMID:11353084

A; Reference number: A99512; MUD:21267165; PMID:11353084

A; Reference mycoplasma pulm

A; Reference DA

A; Residua: preliminary

A; Residua: Decomple type: DNA

A; Residua: Lofo ckUR>

A; Residua: 1-606 ckUR>

A; Experimental source: strain UAB CTIP
F;93,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status F;130/Binding site: carbohydrate (Asn) (covalent) #status predicted F;239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted F;240/Active site: Glu #status predicted F;319-508/Disulfide bonds: #status predicted
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1; Mismatches
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Matches 9; Conservative
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A3332; A32437; A61367
R;Nagayoshi, T.; Sanborn, D.; Hickok, N.J.; Olsen, D.R.; Fazio, M.J.; Chu, M.L.; Knowltc
DNA 8, 581-594, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Human nidogen: complete amino acid sequence and structural domains deduced from A;Reference number: A33322; MUID:90091745; PMID:2574658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-1277 cNAG.
A;Cross-references: UNIPROT:P14543; EMBL:M30269
R;Olsen, D.R.; Nagayoshi, T.; Fazio, M.; Mattei, M.G.; Passage, E.; Weil, D.; Timpl, R.,
Am. J. Hum, Genet. 44, 876-885; 1989
A;Title: Human nidogen: CDNA cloning, cellular expression, and mapping of the gene to ch
A;Reference number: A32437; WUID:89270475; PMID:2471408
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Mymp postition: 1943-1943
C;Superfamily: nidogen; EGF homology; LDL receptor YWTD-containing repeat homology; thyr
C;Keywords: basement membrane; beta-hydroxyasparagine; calcium binding; cell binding; co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:729,819/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted F:756/Cross-link: isopeptide (Gln) (interchain to Lys NG-amino of laminin) #status predi F:1137/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Comment: This protein is a basement membrane glycoprotein that forms a complex
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A; Residues: 667-1247 <0LS>
A; Residues: 667-1247 <0LS>
A; Cross-references: EMBL:A745; NID:g602466; PIDN:AAA57261.1; PID:g602467
A; Note: the authors translated the codon AAG for residue 966 as Cys
R; Fazio, M.J.; O'Leary, J.; Kaehaeri, V.M.; Chen, Y.Q.; Saitta, B.; Uitto, J.
J. Invest. Dermatol. 97, 281-285, 1991
A; Title: Human nidogen gene: structural and functional characterization of the A; Reference number: A61367; MUID:91302882; PMID:1906509
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F:890-1032/Domain: thyroglobulin type I repeat homology <YW
F:990-1032/Domain: LDL receptor YWTD-containing repeat homology <YR
F:1033-1075/Domain: LDL receptor YWTD-containing repeat homology <YR
F:1076-1120/Domain: LDL receptor YWTD-containing repeat homology <YR
F:1121-1197/Domain: LDL receptor YWTD-containing repeat homology <YR
F:121-1243/Domain: LDL receptor YWTD-containing repeat homology <YR
F:1212-1243/Domain: EGF homology <EG6>
F:289,296/Binding site: sulfate (Tyr) (covalent) #status predicted
                                                                                                                                                             Length 606;
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A;Gene: MYPU 1970
A;Genetic code: SGC3
C;Superfamily: Ureaplasma urealyticum hypothetical
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                                                                                                                                                         Score 40; DB 2
Pred. No. 65;
5; Mismatches
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F;714-750/Domain: EGF homology < EG3 >
F;26-260/Domain: EGF homology < EG4 >
F;806-839/Domain: EGF homology < EG5 >
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                                                                                                                                                         58.8%;
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                                                                                                                                                Query Match
Best Local Similarity 50.0
Matches 7; Conservative
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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takai awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; R DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy, A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:O9Y984; DDBJ:AP000064; NID:95105945; PIDN:BAA81416.1; PID:d'A;Experimental source: strain Kl
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Nature 406, 955-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:091108; GB:AE004675; GB:AE004091; NID:g9948522; PIDN:AAG058<sup>c</sup> A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PA2474 [imported] - Pseudomonas aeruginosa (strain PAO1) C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C; Accession: B83336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Aeropyrum pernix
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, submitted to the Protein Sequence Database, March 2000 A;Reference number: Z24374 A;Accession: T47186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 2; Length 252;
Pred. No. 42;
4; Mismatches 2; Indels
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Pred. No. 50;
                                                                                                                                                                                                                                                                                                                            Length 227;
                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein APE2401 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9NSM3; EMBL:AL162032
A;Experimental source: adult testis; clone DKFZp434B1272
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                                                                                                                                                                                                                                                                                                                         Score 39; DB 2; Pred. No. 39; 1; Mismatches
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149 ATALIIPVLLSMP 161
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Best Local Similarity 53.0-
T, Conservative
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113 KAVAVLLPIL 122
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Best Local Similarity
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-252 <KAW>
                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-227 <AAA>
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A;Molecule type: DNA
A;Residues: 1-303 <STO>
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A;Note: DKFZp434B1272.1
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                                                                                                                                                                                                                                                                                        di-N-acetylchitobiase (EC 3.2.1.-) - bovine (fragment)
NyAlternate names: chitobiase; lysosomal glycosidase
NyAlternate names: chitobiase; lysosomal glycosidase
C;Species Bos primigenius taurus (cattle)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Mar-1997
C;Accession: B44102
R;Fisher, K.J.; Aronson Jr., N.N.
J. Biol. Chem. 267, 19667-1967, 1967-1992
A;Title: Cloning and expression of the cDNA sequence encoding the lysosomal glycosidase
A;Reference number: A44102, MUD:92406917; PMID:1527079
A;Accession: B44102
A;Accession: B44102
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-175 <FISA
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIP:113986)
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Vng0274c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Ebe-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84187
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-201 <STO>
A;Cross-references: UNIPROT:Q9HSE2; GB:AE004437; NID:g10579909; PIDN:AAG18865.1; GSPDB:G
C;Genetics:
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C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47186
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     Score 40; DB 1; Length 1247;
Pred. No. 1.3e+02;
2; Mismatches 1; Indels
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Pred. No. 30;
3; Mismatches 3; Indels
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Best Local Similarity 57.1%;
Matches 8; Conservative
     Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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21 RLAPLLLPLLLALP 34
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19 RAAAVLVPVVDAA 31
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Best Local Similarity 69.2
Matches 9; Conservative
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15 ALLIPLLLAGP 25
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A; Status: preliminary
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyx A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: F72554
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <KAM>
                                                                                                                                                             A,Cross-references: UNIPROT:Q9YB75; DDBJ:AP000062; NID:g5105244; PIDN:BAA80723.1; PID:d1
A;Experimental source: strain K1
C;Genetics:
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:QBU966; GB:AE008689; PIDN:AAL44672.1; PID:g17742298; GSPDB:GA;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein Atu3863 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35263
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, April 1999
A;Reference number: Z21573
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A,Reference number: AB2577; WUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Molecule type: DNA
A;Residues: 1-432 <OLI>
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Pred. No. 70;
3; Mismatches
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Pred. No. 63;
1; Mismatches
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Best Local Similarity 61.5%;
Matches 8; Conservative 3
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Best Local Similarity 72.7%;
Matches 8; Conservative
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15 AASLLVPSLLTAP 27
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A;Molecule type: DNA
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phosphate binding protein [imported] - Yersinia pestis (strain CO92)

C; Species: Versinia pestis
C; Species: Versinia pestis
C; Species: Versinia pestis
C; Species: Versinia pestis
C; Accession: ACO389
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-354 < KUR>
A; Residues: 1-354 < KUR>
A; Cross-references: UNIPROT:Q8ZC23; GB:AL590842; PIDN:CAC92438.1; PID:g15981140; GSPDB:CC; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 21
G84971
ompF-like porin [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: G84971
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Accession: G84971
A;Accession: G84971
A;Status: preliminary
A;Accession: G84971
A;Status: preliminary
A;Accession: G84971
A;Essiduse: 1-32 < s7D>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: ompF; BU359
C;Superfamily: outer membrane protein phoE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein APE1722 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1399 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F72554
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
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58;
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Pred. No. 62;
6; Mismatches
  Mismatches
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Pred. No. 5
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40 RSVALVLPVTLASP 53
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RKSLAMVIPMLLAA 17
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96 AEILVPVLLADP 107
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Best Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
8; Conservative
                                                   4 AAVLLPVLLAAP 15
Matches
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                A;Status: preliminary
Modecule type: DNA
A;Residues: 1-602 <KUR>
A;Cross-references: UNIPROT:Q8U966; GB:AE007870; PIDN:AAK89555.1; PID:g15159439; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trypsin/factor XIIa inhibitor precursor - maize
N;Alternate names: Hageman factor inhibitor
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Accession: $20850; A01327
C;Accession: $20850; Mulp:92216060; PMID:1558956
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A; Title: Amino acid sequence and secondary structural analysis of the corn inhibitor of A; Reference number: A01327; WUID: 84239823; PMID: 6610678
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A. Residues: 29-48, 'C', 50-55, 'R', 57-60, 'PR', 61-106,'A', 108-116,'A', 118-119,'Q', 121-134,'
A. Residues: 29-48,'C', 50-55,'R', 57-60,'PR', 61-106,'A', 108-116,'A', 118-119,'Q', 121-134,'
A. Monte: 17-Glu was also found
C; Comment: Five disulfide bonds are present.
C; Superfamily: wheat alpha-amylase inhibitor
C; Superfamily: wheat alpha-amylase inhibitor
F; 1-28/Domain: signal sequence #status predicted <SIG>
F; 29-138/Product: trypsin/factor XIIa inhibitor #status experimental <MAT>
F; 139-155/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F; 62/Inhibitory site: Arg (trypsin) #status experimental
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(Species Saccharomyces cervibiae
(Species Saccharomyces cervibiae
(Species 39-May-1994 #sequence revision 27-Jan-1995 #text_change 09-Jul-2004
(SAccession: 846667; A48424; 846753
(SAccession: 846667; N.M.; Johnson, A.D.
(Genetics 133, 785-797, 1993
(A) Title: A conditional allele of the Saccharomyces cerevisiae HOP1 gene is suppressed by
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Pred. No. 95;
3; Mismatches
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Pred. No. 40;
0; Mismatches
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Best Local Similarity 63.6%;
Matches 7; Conservative
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A, Map position: linear chromosome
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299 AVVAPILIAAP 309
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Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-155 < WEN>
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A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Accession: P90031
A;Accession: P90031
A;Accession: P90031
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-534 <KUR>
A;Cross-references: UNIPROT:Q99RV0; GB:BA000018; PID:g13702123; PIDN:BAB43415.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
A;Genetics:
A;Gen
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                                                                                                                                                                                                                                                                                                                                                                                                         PTS system, arbutin-like IIBC component [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.)Accession: F90031
R.;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; C.; A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001;
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Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
Accession: T51035
                                                            Gaps
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Pred. No. 87;
2; Mismatches 3; Indels
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85;
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                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.4%; Score 39; DB Best Local Similarity 57.1%; Pred. No. 85; Matches 8; Conservative 2; Mismatches
                    ed. No. 79;
Mismatches
                    Pred.
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Best Local Similarity 61.5%;
Matches 8; Conservative 2
                    63.6%;
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302 KKVAALLIPATLTA 315
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                                                            7; Conservative
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190 AVVAPILIAAP 200
                                                                                                                                S AVLLPVLLAAP 15
                    Similarity
                    Best Local
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C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C; Accession: T35589; S37564
Estanders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, August 1998
A; Accession: T3589
A; Accession: Tanslated from GB/EMBL/DDBJ
A; Accession: Tanslated from GB/EMBLAD31317; FIDN:CAA20416.1; GSPDB:GN00070; SCOEI
A; Accession: A.M.; Kieser, K.; Hopwood, D.; Thompson, C.; Mazodier, P.
B; Duchene, A.M.; Kieser, K.; Hopwood, D.; Thompson, C.; Mazodier, P.
A; Description: Molecular characterization of two groEL genes in Streptomyces coelicolor
A; Reference number: S37564
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submitted to the EMBL Data Library, September 1993
A;Description: Induction of chitinases and beta-glucanases in Rhizoctonia solani infecte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-315 <a href="ALM">A; Residues: Residues
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C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chitinase (EC 3.2.1.14) - rice
C;Species: Oryza sativa (rice)
C;Date: 18-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X75206; NID:g406595; PIDN:CAA53017.1; PID:g406596
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A;Molecule type: mRNA
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Pred. No. 62;
2; Mismatches
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0; Mismatches
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Matches 10, Conservative
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A,Molecule type: DNA
A,Residues: 121-249 <DUC>
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                               A; Accession: $4667

A; Residues: 1-182 - 400.

A; Fitle: Characterization of REC104, a gene required for early meiotic recombination in A; Recession: A48424

A; Recession: A48424

A; Recession: A48424

A; Residues: 1-182 - 401.

A; Recession: A64753

A; Recession: A64753

A; Recession: A64753

A; A; Recession: A64753

A; Residues: 1-182 - 401.

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               A; Reference number: 846667; MUID:93216080; PMID:8462842
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hypothetical protein T26H5.1 - Caenorhabditis elegans
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Pred. No. 61;
4; Mismatches
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Pred. No. 46;
2; Mismatches
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ilarity 46.2%;
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140 AVTFMIPIILAAP 152
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Matches

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C;Accession: JC4802
R;Lee, J.K.; Kim, Y.O.; Kim, H.K.; Park, Y.S.; Oh, T.K.
Biosci. Biotechnol. Biochem. 60, 840-846, 1996
A;Title: Purification and characterization of a thermostable alkaline protease from Thereshoes number: JC4802; MUID:96261070; PMID:8704314
A;Reference number: JC4802
A;Molecule type: DNA
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A;Cross-references: UNIPROT:Q56365; GB:U31759; NID:gl389689; PIDN:AAB36499.1; PID:g1683*
A;Experimental source: strain E79
C;Comment: This protein is thermostable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: extracellular alkaline serine proteinase [validated, MUID:96261070]
C; Superfamily: subtilisin; subtilisin homology
C; Superfamily: subtilisin; subtilisin predicted cs.
C; State in Marolase; serine proteinase
F; 1-25; Domain: signal sequence #status predicted cs.
F; 26-106; Domain: propeptide #status predicted cs.
F; 26-106; Domain: propeptide #status predicted cs.
F; 24-34; Domain: subtilisin homology cs.
F; 314-34; Domain: subtilisin homology cs.
                                                                                                                                                                                                                                          alkaline proteinase (EC 3.4.21.-) precursor - Thermoactinomyces sp. (strain B79) C; Species: Thermoactinomyces sp. A; Variety: strain B79 C; Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
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Pred. No. 92;
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4 KVLALLIPALLAA 16
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Best Local Similarity
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C; Species: Escherichia coli
C; Species: Dscherichia coli
C; Species: L2-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C; Accession: D64808
R; Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1397
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Rose, D.J. 1462, 1397
A; Tetrerence number: A64720; MUID:97426617; PMID:9278503
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Retres: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Resterences: UNIPROT:P77747; GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74459.
A; Experimental source: strain K-12, substrain MG1655
C; Superfamily: outer membrane protein; poen;
F; L-21/Domain: signal sequence #status predicted <SIG>F; 22-377/Product: probable outer membrane porin b1377 #status predicted <OPP>
                            A;Accession: S39979
A;Status: preliminary
A;Status: preliminary
A;Residus: 1-339 «NIS»
A;Cross-references: UNIPROT:Q43294; EMBL:X56787
A;Cross-references: UNIPROT:Q43294; EMBL:X56787
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;33-74/Domain: hevein chitin-binding domain homology «HCB»
F;91-329/Domain: plant chitinase homology «PCH»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Reference number: $40414

A; Reference number: $40414

A; Accession: $40414

A; Status: presiminary

A; Molecule type: MRNA

A; Residues: 1-340 «NIS>

A; Cross-references: UNPROT:043284; EMBL:X56787; NID:9407471; PIDN:CAA40107.1; PID:94074

A; Cross-references: UNPROT:043284; EMBL:X56787; NID:9407471; PIDN:CAA40107.1; PID:94074

C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C; Keywords: 91ycosidase; hydrolase; polysaccharide degradation

C; Keywords: 91ycosidase; hydrolase; polysaccharide degradation

F; 33-74/Domain: hevein chitin-binding domain homology «HCB»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chitinase (EC 3.2.1.14) - rice
C;Species: Oryza sativa (rice)
C;Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 377;
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Pred. No. 82;
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A; Reference number: S39979; MUID: 94049667; PMID: 7901749
                                                                                                                                                                                                                                                                                                                                                                                                           4;
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R,Nishizawa, Y.
submitted to the EMBL Data Library, November 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB
Pred. No. 90;
2; Mismatches
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Best Local Similarity 71.4%;
Matches 10; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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Gaps

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C;Dāte: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
A;Accession: A9664
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNR Res. 8, 11-22, 2001
DNR Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli Ol57:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q8X959; GB:BA000007; PIDN:BAB33544.1; PID:g13359577; GSPDB:G.C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable membrane protein yacH [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli
B; Specia M.T.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew R; Perna, N.T.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A,Residues 1.617, cSTO-
A;Cross-references: UNIRROT:Q8X959; GB:AE005174; NID:g12512829; PIDN:AAG54421.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                               probable membrane protein [imported] - Escherichia coli (strain 0157:H7, substrain RIMD C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Y57AlOA.ff - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T31653
R;Smye, R.
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Pred. No. 1.4e+02;
2; Mismatches 3;
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C;Superfamily: Escherichia coli yacH protein
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C;Superfamily: Escherichia coli yacH protein
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Best Local Similarity 61.5%;
Matches 8; Conservative ;
                                 15
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50 AAAVTLPATVSAP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AAAVLLPVLLAAP 15
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Matches 8; Conservative
                              1 KKAAAVLLPVLLAAP
                                                                                    42 KAAVLVLLTALVAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
Residues: 1-617 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Status: preliminary
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A;Nolecule type: DNA
A;Residues: 1-601 - KURS
A;Esperimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
B;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Genetics:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable ABC-type iron transport system protein SMa0525 [imported] - Sinorhizobium melil C; Species: Sinorhizobium meliloti C; Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C; Ascession. E95296 R; Barnett, M.J.; Pisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows F.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. A; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. A; Tille: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A; Recession: E95296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: UNIPROT: Q9ZBPO; EMBL: AL034492; PIDN: CAA22503.1; GSPDB: GN00070; SCOED
                                                                                                                                                                                                                                                                                                                                                                                                                                probable regulatory protein - Streptomyces coelicolor
Gispecies: Streptomyces coelicolor
Cjaccession: 135476
KiOliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Bubmitted to the EMBL Data Library, December 1998
A;Reference number: Z21579
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reteus preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-569 <OLI>
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                           A;Gene: XF1992
C;Superfamily: Azospirillum cyclohydrolase II; cyclohydrolase homology
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                                                                                                         Score 38; DB 2; Length 398;
Pred. No. 95;
3; Mismatches 1; Indels
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Pred. No. 1.4e+02;
1; Mismatches 5; Indels
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Pred. No. 1.3e+02;
0; Mismatches 3;
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                                                                                                               Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 AAPVLLPGLGAAP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AAAVLLPVLLAAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 76.9
Matches 10; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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131 ALLLPAIVAAP 141
                                                                                                                                                                                                                                  5 AVLLPVLLAAP 15
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A;Genome: plasmid
C, Genetics:
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Gaps

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Gape

Page 16

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A percription: accepts electrons from cytochrome-c3 hydrogenase (EC 1.12.2.1) and trans?
A pethway: sulfate respiration
A pethway: sulfate respiration
C superfamily: Cytochrome c3; cytochrome c3; homology
C; Superfamily: Cytochrome c3; electron transfer; heme; iron; metalloprotein; sulfate respiralization cytochrome c3 #status experimental cMAT>
F; 24-130/Product: cytochrome c3 #status experimental cMAT>
F; 37-120/Domain: cytochrome c3 #status experimental cMAT>
F; 37-120/Binding site: heme iron (His) (axial ligands) #status experimental
F; 35, 35/Binding site: heme iron (His) (axial ligands) #status experimental
F; 69, 74/Binding site: heme (Cys) (covalent) #status experimental
F; 91, 122/Binding site: heme (Cys) (covalent) #status experimental
F; 102, 105/Binding site: heme (Cys) (covalent) #status experimental
F; 102, 105/Binding site: heme (Cys) (covalent) #status experimental
F; 123, 128/Binding site: heme (Cys) (covalent) #status experimental
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C;Species: Acaracterium tumefaciens
C;Species: O: Acaracterium tumefaciens
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I krwood, D.W.; Setubal, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
R; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9RXG9; GB:AE001894; GB:AE000513; NID:g6458011; PIDN:AAF099.
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                           residues 24-64,'N',66-130
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.S.; Smith, H.O.; Venterr, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A55250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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                                                                  A;Contents: annotation; X-ray crystallography, 1.8 angstroms R;Higuchi, Y.; Kusunoki, M.; Matsuura, Y.; Yasuoka, N.; Kakudo, submitted to the Brookhaven Protein Data Bank, November 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 130;
Pred. No. 50;
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                                                                                                                                                                                       A;Reference number: A50415; PDB:2CDV
A;Contents: annotation; X-ray crystallography, 1.8 angstroms, C;Function:
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60.0%; Pred. No. 74;
tive 2; Mismatches
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Best Local Similarity 53.8
Matches 7; Conservative
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A;Status: preliminary
A;Molecule type: DNA
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A;Reference number: 221607
A;Accession: T36946
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-776 <SEE>
A;Cross-references: UNIPROT:Q9RJ01; EMBL:AL109962; PIDN:CAB53131.1; GSPDB:GN00070; SCOED A;Gene: SCOEDB:SCJ1.13
submitted to the EMBL Data Library, September 1999
A;Reference number: 221048
A;Accession: T31653
A;Access
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R; Kitamura, M.; Ozawa, K.; Kojima, S.; Kumagai, I.; Akutsu, H.; Miura, K.
Protein Seq. Data Anal. 5, 193-196, 1993
A; Title: The primary structure of pre-cytochrome c(3) from Desulfovibrio vulgaris (Miyaz A; Reference number: 833874
A; Accession: 833874
A; Accession: 833874
A; Accession: 833874
A; Residues: 1-130 «KIT>
A; Residues: 1-130 «KIT>
A; Residues: 1-130 «KIT>
A; Residues: 1-130 «KIT>
A; Rillia Mino acid sequence of cytochrome c-3 from Desulfovibrio vulgaris, Miyazaki.
A; Rillia Mino acid sequence of cytochrome c-3 from Desulfovibrio vulgaris, Miyazaki.
A; Reference number: A00125; MUID: 80249474; PMID: 6249799
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C,Species: Desulfovibrio vulgaris
C,Date: 31-Oct-1980 #sequence_revision 10-Oct-1997 #text_change 09-Jul-2004
C,Accession: S33874; A00125
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Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Accession: T36946
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A;Molecule type: protein
A;Residues: 24-64, N',66-130 <SHI>
R;Higuchi, Y.; Kusunoki, M.; Matsuura, Y.; Yasuoka, N.; Kakudo, M.
J. Mol. Biol. 172, 109-139, 1984
A;Title: Refined structure of cytochrome c-3 at 1.8 angstrom resolution.
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F;442-585/Domain: ATPase nucleotide-binding domain homology <ATN>
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Pred. No. 2.3e+02;
1; Mismatches 3; Indels
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Pred. No. 2.1e+02;
3; Mismatches 1;
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270 RAVAVLVVATPCPLLLAAP 288
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Best Local Similarity 52.6%;
Matches 10; Conservative
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Best Local Similarity 69.2%;
Matches 9; Conservative
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200 AAAPSPPILLAAP 212
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Mismatches

3;

8; Conservative

Matches

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hypothetical protein 24219 [imported] - Escherichia coli (strain 0157:H7, substrain EDL9
C.Species: Escherichia coli
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                           C;Accession: E85943
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q46813; GB:AE005174; NID:g12517404; PIDN:AAG58009.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein b2880 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: 12-Sep.1997 #sequence_revision 17-Sep.1997 #text_change 09-Jul-2004
C;Date: 12-Sep.1997 #sequence_revision 17-Sep.1997 #text_change 09-Jul-2004
C;Jaccesion: H65071
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y.
A; Rose, D.J.; Mau, B.; Shao, Y.
A;Tile: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A;Residues: 1-29, <BLAT>
A;Cross-references: UNIPROT: 046813; GB:AE000371; GB:U00096; NID:g1789239; PIDN:AAC75918.
A;Experimental source: strain K-12, substrain MG1655
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Pred. No. 94;
3; Mismatches
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Pred. No. 94;
3; Mismatches
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Job time: 23.7188 secs
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Best Local Similarity 61.5%;
Matches 8; Conservative
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110 RQEESVLLPVLLA 122
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110 RQEESVLLPVLLA 122
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110 RQEESVLLPVLLA 122
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Best Local Similarity 61.5
Matches 8; Conservative
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Ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Accession: AC2793

A;Status: preliminary

A;Status: preliminary

A;Status: preliminary

A;Status: DNA

A;Residues: 1-254 <KIRN>

A;Cross-references: UNIPROT;Q8UEJ5; GB:AE008688; PIDN:AAL42761.1; PID:g17740203; GSPDB:GCGenetics:

A;Experimental source: strain C58 (Dupont)

A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: circular chromosome
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hypotherical protein AGR C 3235 [imported] - Agrobacterium tumefaciens (atrain C58, Cere C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97572

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2321-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MuID:21608551; PMID:11743194
A;Accession: A97572
A;Accession: A97572
A;Residues: 1-254 «KUR»
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hypothetical protein EC83753 [imported] - Escherichia coli (strain O157:H7, substrain RI Cispeciaes Escherichia coli
Cispeciaes Escherichia coli
Cibate: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 09-Uul-2004
CiAccession: A98098
Rihayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99098
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q8UEJ5; GB:AE007869; PIDN:AAK87530.1; PID:g15156862; GSPDB:q
C;Genetics:
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A;Cross-references: UNIPROT:Q46813; GB:BA000007; PIDN:BAB37176.1; PID:g13363225; GSPDB:G
A;Expensed: Source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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Pred. No. 94;
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A;Map position: circular chromosome
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STRAIN=CGA009 / ATCC BAA-98;
STRAIN=CGA009 / ATCC BAA-98;
PubMeda14704707; DOI=10.1038/nbt923;
Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
Harrison F.H., Glabon J., Harwood C.S., Torres y Torres G.,
"Complete genome sequence of the metabolically versatile
photosynthetic bacterium Rhodopseudomonas palustris.";
MAL. Biotechnol. 22:55-61(2004).
EMBL, BXS72593; CAR256721; .
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzeae; Oryza, Liliopsida; Poales; Poaceae;
CORJE_TaxID=39947;
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                                               Rhodopseudomonas palustris.
ascieria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
NCBI_TaxID=1076;
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Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski
Currie J., Collura K.;
Submited (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC099399; AAN05509.1; --
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GO, GO:0016998; Prcell wall catabolism; IEA.
GO; GO:0016998; Prcell wall
Interpro; IRR002482; LyBM.
Pfam; PF01476; LyBM; 2.
SMART; SM00257; LyBM; 2.
Hypothetical protein.
SEQUENCE 356 AA; 37200 MW; 007D7BED10AB98FE CRC64;
                                                                                                                                                                                                                                                                                                                                SEQUENCE 133 AA; 14481 MW; E22F622199718B5B CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
10-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein OJ1006F06.19.
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein precursor.
OrderedLocusNames=RPA0228;
                                                                                                                                                                                                                                                                                                                                                              66.2%; Score 45; DB 2; 78.6%; Pred. No. 15; iive 0; Mismatches
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1; Mismatches
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Q6X233
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Q830V6
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CAPP RALSO
Q8FMEO
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Q9VW60
Q8C0S4
Q9D5Q9
SOS1 MOUSE
Q8BPB6
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FMT_CAUCR
Q8A1Q2
GP62_HUMAN
Q8TAM0
Q7N159
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PSBY GUITH
Q6DFA9
085873
06TEC0
Q9GNP1
Q87V39
Q75IL7
Q75IL8
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Q8ABD0
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Q88PQ5
Q69N36
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Q6ND81;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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QGNZWZ QGNZWZ;

Created) Last sequence update) 133 AA.

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RESULT 1 Q6ND81

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"Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
Putative iron transport membrane protein.
OrderedLocusNames=CB0685;
Corymbacterium efficiens.
Bacteria, Actinobacteria, Actinobacteriaes;
Corymebacterinese; Corymebacterinese; Corymebacterium.
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Borrell-Pages M., Arribas J.;

Bornell-Pages M., Arribas J.;

Bornell-Pages M., Arribas J.;

Bubli, AP3066612, AR34676.2; -.

HSSP; P50281; 18Q0.

MEROPS; MIO.014; -.

GO, GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.

GO; GO:0004222; F:metalloendopeptidase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000585; Hemopaxin.
                                                                                                                                                                                                                                                    STRAIN=YS-314;
MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E. Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 13.1572-1579(2003).
EMBL; AP005216; BAC17495.1; -.
HSSP; P06609; 1L/TV.
GO; GO:00160215; Firansporter activity; IEA.
GO; GO:0006810; P:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000522; FecD.
Pfam; PP01032; FecCD; 1.
Complete proteome.
SEQUENCE 340 AA; 34818 MW; 14B047C6A943A57
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100.0%; Pred. No. 75;
ive 0; Mismatches
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InterPro; IPR001818; Pept M10A M12B.
InterPro; IPR008025; Pept M Zn_BS.
InterPro; IPR009070; PGBD_1Tke.
Pfam; PF00045; Hemopexin; 4.
Pfam; PF0333; Peptidase M10_N; 1.
PRINTS; PR00138; MATRIXIN.
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STRAIN=RIMD 2210633 / Serotype O3:K6;

STRAIN=RIMD 2210633 / Serotype O3:K6;

STRAIN=225086454; Pubmed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

MREDLINE=225086454; Pubmed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

Makino K., Oshima M., Kirokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CGA009 / ATCC BAA-98;
BubMed=14704707; DOI=10.1038/nbt923;
BubMed=14704707; DOI=10.1038/nbt923;
Busmer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L. Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";
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                                                                                                  Rhodopseudomonas palustris.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Bradyrhizobiaceae, Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.2%; Score 43; DB 2; Length 190; 60.0%; Pred. No. 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 AA; 54125 MW; 6A764989856F441B CRC64;
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               05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
62-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein precursor.
OrderedLocusNames=RPA3936;
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24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Hypothetical protein; Signal.
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(TrEMBLrel. 27, Created)
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EMBL; BX572605; CAE29377.1; -.
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103 KQAAKVVTPVSMAAP 117
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Matches 9; Conservative
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19 AAIVLPVVLAA 30
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Best Local Similarity
                                                                                                                                                               NCBI_TaxID=1076;
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Q87TJ5

RESULT 4
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Indels

SKRRRS

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RESULT 7 Q6AA99

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SEQUENCE FROM N.A.

STRAIN=RBSO / ATCC BAA-588;

MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

MATAIN=RBSO / ATCC BAA-588;

MATAIN=RBSO / ATCC BAA-588;

MATAIN=RBSO / ATCC BAA-588;

MATAIN J., Schaina M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chrimman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., Relucal T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J., Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapartussis, and Bordetella bronchiseptica.",
                 MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
Rarkhill J., Sebaihia M., Preston A., Murphy L.D., Thombon N.R.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chilingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Ablindingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
Rabbinowitech E., Rutter S., Sanders B., Seeger K.,
Abbinowitech E., Rutter S., Sanders R., Squares S., Stevens K.,
Normparative analysis of the genome sequences of Bordetella pertussis,
Nat. Genet. 35:32-40(2003).
BMBL; Bx640435, CAB3925-1; -.
BMBL; Bx640435, CAB3925-1; -.
BMBL; Bx640435, CAB3925-1; -.
RIGRAMS, TIGRODSS2; UPF0102; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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Pred, No. 61;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 2; Length 177;
Pred. No. 61;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        177 AA; 19268 MW; 2A1BDFD4964FFBBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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EMBL; BX64840; CAE34878.1; -.
InterPro; IPR003509; UPF0102.
Pfam; PF02021; UPF0102; 1.
TIGRFAMS; TIGR00252; UPF0102; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.8%;
81.8%;
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81.8%;
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Best Local Similarity 81.0.,
Best Local 9, Conservative
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OrderedLocusNames=BB4515;
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115 RAAALLLPVLL 125
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 177 AA;
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SEQUENCE 177 AA.
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PubMed=15286373; DOI=10.1126/science.1100330;
Brueggemann H., Henne A., Hoster F., Liesegang H., Wiezer A.,
Strittmatter A., Huler S., Duerre P., Gottschalk G.;
"The complete genome sequence of Propionibacterium acnes, a commensal
of human skin.";
of human skin.";
Science 305:671-673(2004).
EMBL; AR0172318.1;
InterPro; IPR008928; Glyco trans 6hp.
InterPro; IPR008928; Glyco trans 6hp.
InterPro; IPR008928; Peptidase Mi4.
InterPro; IPR000845; Peptidase Mi4.
InterPro; IPR001085; Pepticys_acsite.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Propionibacterineae, Propionibacterium.NCBI_TaxID=1747;
                                                                                                                                                      Length 582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.2%; Score 43; DB 2; Length 671; 64.3%; Pred. No. 1.4e+02; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                Indels
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                                                                                                           66068 MW; 390ECAA632D32DF8 CRC64;
                                                                                                                                  DB 2; Leus
). 1.2e+02;
0;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Conserved protein containing thioredoxin domain.
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Last annotation update)
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PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                             671 AA.
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SMART; SM00235; ZnMc; 1.
PROSITE; PS00546; CYSTEINE SWITCH; 1.
PROSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
MELALLOpiccease; Protease.
SEQUENCE 582 AA; 66068 MW; 390ECAA632D3:
                                                                                                                                                 63.2%; Score 43; DB 100.0%; Pred. No. 1.2
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                                                                                                                                               Query Match
Best Local Similarity 100.'
Matches 10; Conservative
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                 539 AAAVLLPVLL 548
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                                                                                                                                                                                                                                         3 AAAVLLPVLL 12
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SEQUENCE FROM N.A.
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SEQUENCE 671 AA
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STRAIN=MARF30309;
MEDLINE=21082930; PubWed=11214968;
MEDLINE=21082930; PubWed=11214968;
Maneko T., Nakamura Y., Sato Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Makayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=11310 / Biovar 1;
MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodgon R.J., Nayam L.A., Brinkac L.M., Beanan M.J.,
Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mlr3636 protein.
OrderedLocusNames=mlr3636;
Rhizobium loti).
Bacteria: Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                       Length 260;
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                                                                                                                                                                                                                                                       0; Indels
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   GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR002781; DUF81.
Pfam; PF01925; DUF81; L.
Complete proteome; Hypothetical protein; Transmembrane.
SEQUENCE 260 AA; 28137 MW; 8CFC59D49FF07A65 CRC64;
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SEQUENCE 291 AA; 31162 MW; 3C6E651E33A79EE2 CRC64;
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Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNI-2003 (TrEMBLrel. 24, Last annotation update)
Membrane protein, putative.
OrderedLocusNames=BR1873;
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                                                                                                                                                                                       Score 42; DB 2
Pred. No. 87;
4; Mismatches
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EMBL; AP003002; BAB50490.1; -.
                                                                                                                                                                                          61.8%;
66.7%;
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Matches 8, Conservative
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45 QAAALLLPILIA 56
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                                                                                                                                                                                                                                                                                                             2 KAAAVLLPVLLA 13
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NCBI TaxID=29461;
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Matches 7, Conserv
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Q98FS7
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Wu M., Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,

Wu M., Sun L.V., Wordraw E.A., Martin W., Esser C., Ahmadinejad N.,

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a streamlined genome overrun by mobile genetic elements.";

EMBL, AE017257; A&14173.1;

TIGR; WD0452.
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MEDLINE-21396507;
PUBDLINE-21396507;
MEDLINE-21396507;
MEDLINE-21396507;
MEDLINE-21396507;
MEDLINE-21396507;
Mape F., Batut J.,
Gapela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Kahn D., Kiss E., Lelaure V., Maeuy D.,
Ronla T., Goffeau A., Kahn D., Kiss E., Lelaure V., Maeuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
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Analyais of the chromosome sequence of the legume symbiont
Sinorhizobium melloti strain 1021.";
EPPC. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachia.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLREL. 23, Last annotation update)
01-MAR-2003 (Sinorhizobium meliloti)
Rhizobium meliloti (Sinorhizobium meliloti).
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TAXID=382;
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Last annotation update)
                                                                                                                                                                                       253 AA
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                                                                                                                                                                                    PRT;
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InterPro; IPR002033; Translocase.
Pfam; PF00902; TaCC; 1.
PRINTS; PR01840; TATCFAMILY.
TIGRFAMs; TIGR00945; tatC; 1.
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
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                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 2
MttB family protein.
OrderedLocusNames=WD0452;
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Matches 9; Conservative
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115 RAMALLEPVLL 125
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05-JUL-2004
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OrderedLocusNames=BB1095;
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                                                                                                   NCBI_TaxID=518;
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STRAIN=16M / ATCC 23456 / Biotype 1;

STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N.C., Overbeek R.; The genome sequence of the facultative intracellular pathogen Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
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Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
Van Aken S.B., Riedmuller S., Tettelin H., Gill S.R., White O.,
Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
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81.8%; Pred. No. 98;
iive 2; Mismatches 0; Indels
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Pred. No. 97;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                293 AA; 30733 MW; 4DFD4347112050AE CRC64;
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Last annotation update)
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InterPro; IPR00620; DUF6.
Pfam; PF00892; DUF6; 1.
Complete Protecome.
SEQUENCE 293 AA; 30733 MW; 4
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GO; GO:0016020; C:membrane; IEA.
Pfam; PF00892; DUF6; 1.
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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Brucella melitensis.
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Best Local Similarity 81.8
Matches 9; Conservative
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156 AAALLIPVLLA 166
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Q7WNES;
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Q7WNE5
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REPUENCE FROM N.A.

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SECURINE-2282-954; PubMed=12910271; DOI=10.1038/ng1227;

REPLAINE-228-954; PubMed=12910271; DOI=10.1038/ng1227;

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RADENTH M., Atkin R., Baker S., Bames K.D., Harris B., Quall M.A.,

RADENTH J., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

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ROMPATALIVE S., SIRMONGS and Bordetella bronchiseptica.";

REL, BX640440; CAB31593.1; -

REL, BX640440; CAB31593.1; -

REL, BX640440; CAB31593.1; -

REL, PV34041; Bugi 1.

RW FEMB., PV3401; Bugi 1.

RW Complete proteome.

SQUENCE 323 AA, 34109 MW, 9AD672EE48F646E4 CRC64;
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Eradyrhizobium japonicum USDAIIO.";
DNA Res. 9:189-197(2002).

E MBL, APO05956; BAC51204-1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; F:transporter activity; IEA.
GO; GO:0006515; F:transporter activity; IEA.
GO; GO:0006516; F:transporter activity; IEA.
InterPro; IPR010645; DUF1228.
E InterPro; IPR007114; MFS.
R PROSITE; PS50850; MFS; 1.
Complete proteome.
Complete proteome.
OCOMPLETE RS50850; MFS; 1.
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MEDLINE-22484998; PubMed-12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Alcaligenaceae, Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blr5939 protein.
OrderedicousNames=blr5939;
Bradyrhizoblum japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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Last annotation update)
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60.0%;
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Query Match
Beet Local Similarity 60.00,
Beet Local Similarity 60.00,
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2 KRYAGILLGMLLAAP 16
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us-10-764-235-2.rup

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Q9BIH2
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
05-JUN-1998 (TrEMBLrel. 27, Last amnotation update)
05-JUN-2004 (TrEMBLrel. 27, Last amnotation update)
14-200-2014 (TremBlrel. 27, Last amnotation update)
Name=F24J7.50; Synonyms=AT4g19490;
Name=F24J7.50; Synonyms=AT4g19490;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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TISSUE=Wing;
MEDLINE=95291280; PubMed=7773253; DOI=10.1016/0965-1748(94)00056-N;
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Neoptera, Orthopteroidea, Orthoptera, Caelifera, Acridomorpha,
Acridoidea, Acrididae, Oedipodinae, Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Vitale D., Liguori R., Argiriou A., De Simone V., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bevan M., Vitale D., Liguori R., Argiriou A., De Simone V., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                         Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.8%; Score 42; DB 2; Length 939; 69.2%; Pred. No. 2.8e+02; ive 2; Mismatches 2; Indels
Score 42; DB 2; Length 422
Pred, No. 1.46+02;
3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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Hypothetical protein.
SEQUENCE 939 AA; 102496 MW; 9DAEBA3F6105CEEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; ALO21768; CAA16526.1;
EMBL; ALO1551; CAB78951.1; -.
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                                                                                                                                                                                                                                                                          939 AA.
                     Query Match
61.8%; Score 42; DB
Best Local Similarity 64.3%; Pred. No. 1.4e
Matches 9; Conservative 2; Mismatches
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                                                                                                                                     311 EAAAVLEPTVSTAP 324
                                                                                                                2 KAAAVLLPVLLAAP 15
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Best Local Similarity 69.4
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CU65_LOCMI
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Krogh T.N., Skou L., Roepstorff P., Andersen S.O., Hoejrup P.;
"Primary structure of proteins from the wing cuticle of the migratory locust, Locusta migratoria.";
Insect Biochem. Mol. Biol. 25:319-329(1995).
-!- FUNCTION: Component of the cuticle of migratory locust which contains more than 100 different structural proteins.
-!- DOMAIN: The tetraseptide (A.A.P.-[AV]) repeats found throughout the protectin are also present in many proteins constituting the protective envelope of other species.
-!- MASS SPECTROMETRY: WM=13319.9; METHOD=Electrospray; RANGE=1-145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gарв
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                    NOTE=Ref.1.

Cuticle; Direct protein sequencing; Repeat; Structural protein. REPEAT 30 1.

REPEAT 39 42 3.

REPEAT 39 42 3.

REPEAT 92 95 5.

REPEAT 98 101 6.

REPEAT 123 126 7.
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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EMBL; AAAB01008844; EAA05987.2; -.
Interpro; IPRO01969; PEPTEASE; UNKNOWN 1.

SEQUENCE 195 AA; 20951 MW; 3DF52FD0418AF6A7 CRC64;
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Last sequence update)
Last annotation update)
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09BIH2;
01-JUM-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein 9SG10 precursor.
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64.3%; Pred. No. 75;
iive 1; Mismatches
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98;
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Pred. No.
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KVAAVAAPVAVAAP 94
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13 SAAVLLQPLLAAP 25
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Les 10; Conservative
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SEQUENCE FROM N.A.
STRAIN=PEST;
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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Q7U481;
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A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye F., Hennequin C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Lewir I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozfar-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
T. "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kluyveromyces lactis strain NRRL Y-1140 chromosome B of strain NRRL Y-
                                                                                                                                                                                        MEDLINE-22257806; PubMed=12062411; DOI=10.1016/S0014-5793(02)02578-4; Lanfrancotti A., Lombardo F., Santolamazza F., Veneri M., Castrignano T., Coluzzi M., Arca' B.; "Novel cDNAS encoding salivary proteins from the malaria vector Anopheles gambiae."; PEBS Lett. 517:67-71(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
       Anophēles gambiae (African malaria mosquito).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=7165;
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Saccharomycetales, Saccharomycetaceae, Kluyveromyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ302660; CAC35525.1; -Interpret; IPR001959; Pept, Agp AS. PROSITE; PS00141; ASP PROFEASE; UNKNOWN_1. Hypothetical protein; Signal.
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SEQUENCE 195 AA; 20951 MW; 3DF52FD0418AF6A7 CRC64;
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ORFNames=KLLA0E02706g;
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13 SAAVLLQPLLAAP 25
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Best Local Similarity 76.9
Matches 10; Conservative
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STRAIN=NRRL Y-1140;
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STRAIN=NRRL Y-1140;
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MEDLINE-21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
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69.2%; Pred. No. 1.18+02;
ive 1; Mismatches 3; Indels
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Complete proteome, Hypothetical protein.
SEQUENCE 231 AA, 24714 MW, 63025D8F4F9A7FC2 CRC64;
                                                                                                                                               222 AA; 24084 MW; 1CAC420F75DA49EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=SYNW2190;
Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                   60.3%; Score 41; DB 2; I 64.7%; Pred. No. 1.1e+02;
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EMBL; CR382125; CR099157.1; -...
InterPro; IPR000504; RNA_rec_mot.
Pfam; PP00076; RRM 1; 1.
SMART; SM00360; RRM; 1.
SMOSITE; PS50102; RRM; 1.
SEQUENCE 222 AA; 24084 MW; 1CAC
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                                                                                                                                                                                                                                                                                                                                                  49 KKAASAALVPALLRAP 65
                                                                                                                                                                                                                                                                                                                  1 KKA--AAVLLPVLLAAP 15
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01-UUN-2003 (TrEMBLrel. 24,
01-UUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
Putative secreted amidase.
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                                                                                                                                                                                             Query Match
Best Local Similarity 64.79
Matches 11, Conservative
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Matches 9; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 metabolizing enzyme activity. Component of the core of photosystem II (By similarity). SUBCELLULAR LOCATION: Cellular thylakoid membrane. SIMILARITY: Belongs to the psbY family.
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STRAIN-BALB/c; TISSUE-Uterus;
STRAIN-BALB/c; TISSUE-Uterus;
Ulrich R., Gerhauser I., Seeliger F., Baumgaertner W., Alldinger S.;
"Expression profile of matrix-metalloproteinases and their inhibitors in actue and chronic demyelinating Theiler's murine encephalomyelitis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                              MEDLINE=2225144; PubMed=12240834;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kishida W., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002).
--- FUNCTION: Manganese-binding polypeptide with L-arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; ME_00717; -; 1.
InterPro; IRPR009388; PsbY.
Pfam; PF06228; PsbY; 1.
Complete proteome; Photosynthesis; Photosystem II; Thylakoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 43;
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                                                          Name=psbY; OrderedLocusNames=ts10836;
Synechococcus elongatus (Thermosynechococcus elongatus)
                                                                                                  Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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B12F8F16EF2EDF86 CRC64;
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Pred. No. 36;
1; Mismatches
  (Rel. 42, Last sequence update) (Rel. 44, Last annotation update)
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[2]
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69.2%;
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43 AA; 4773 MW;
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                                         Photosystem II protein Y.
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Best Local Similarity
                                                                                                                                                            SEQUENCE FROM N.A.
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                    05-JUL-2004
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                                                                                         Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005026; BAC6948-11;
GO; GO:0009745; F:N-accetylumramcyl-L-alanine amidase activity; IEA.
GO; GO:0009753; P:peptidoglycan catabolism; IEA.
InterPro; IPR005502; Amidase_2.
Fam; PF001510; Amidase_2.
Fam; PF001510; Amidase_2.
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Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Maudua S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
"Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix Kl.";
DNA Ree. 68 33-101 (1999).
PIR; D72482; D72482.
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1172aa long hypothetical antibiotic transport-associated protein.
OrderediocusNames=APE2500;
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Pred. No. 3e+02;
3; Mismatches 1; Indels
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SEQUENCE 1172 AA; 124325 MW; 974421D7A4E470D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                            70218 MW; BA3905045D2792FF CRC64;
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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                                                          STRAIN=MA-4680;
MEDLINE=22608306; PubMed=12692562;
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QBDKM3;
10-OCT-2003 (Rel. 42, Created)
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                                                                                                                                                                                                                                                                                                                                                                                 69.28;
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848 KAAPVLLPLLVVA 860
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Best Local Similarity 69.2.
Best Local 9; Conservative
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26 SAALLLPLLGAAP 38
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1es 9; Conservative
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                                                                                                                                                                                                                                                                                                                                              659 AA;
                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                       Complete proteome
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01-NOV-1999
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Q9Y8Y4

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RESULT 25 PSBY_SYNEL

Best Loc Matches

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Gaps

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NCBI_TaxID=394;
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Q854U6;
01-JUN-2003
DISULFID
DISULFID
CONFLICT
SEQUENCE
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Q6W1Z2;
                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    Eur. J. Biochem. 166:387-391(1987).
    -1- FUNCTION: Plant nonspecific lipid-transfer proteins transfer phospholipids as well as galactolipids across membranes. May play a role in wax or cutin deposition in the cell walls of expanding epidermal cells and certain secretory tissues.
    -1- SIMILARITY: Belongs to the plant LTP family.

                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Bernhard W.R., Thoma S., Botella J., Somerville C.R., Isolation of a CDNA clone for spinach lipid transfer protein and evidence that the protein is synthesized by the secretory pathway.", Plant Physiol. 95:164-170(1991).
                                                                                                                                                                                                                                                                                                                                        Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Caryophyllales, Amaranthaceae, Spinacia.
VCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bouillon P., Drischel C., Vergnolle C., Duranton H., Kader J.-C.;
"The primary structure of spinach-leaf phospholipid-transfer
                                                                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Created)
01-JUL-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Nonspecific lipid-transfer protein precursor (LTP) (Phospholipid transfer protein) (PLTP).
Spinacia oleracea (Spinach).
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InterPro; IPR001512; AAI.
InterPro; IPR000528; Plant LTP.
Pfant PR0034; Tryp alpha amyl; 1.
PRINTS; PR0034; ILPIDTRNSFER.
SWART; SM00499; AAI; 1.
PR0SITE; PS00597; PLANT LTP; 1.
PR0SITE; PS00597; PLANT LTP; 1.
2 SIGNAL.
STRAIN=BALB/c; TISSUE-Uterus;
Ulrich R.G., Seeliger F., Alldinger S., Baumgaertner W.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY622974; AAT46405.1; -
                                                                                                   DB 2; Length 67;
54;
                                                                                                                             0; Indels
                                                                          67 AA; 7104 MW; 52CDDDF3957E3FBA CRC64;
                                                                                                                                                                                                                                          117 AA
                                                                                                                           1; Mismatches
                                                                                                    Score 40;
                                                                                                                                                                                                                                         PRT;
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                                                                                                   58.8%;
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                                                                                                Query Match
Best Local Similarity 90.0
Matches 9, Conservative
                                                                                                                                                                                                                                          STANDARD;
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53 AAAVVLPVLL 62
                                                                                                                                                    3 AAAVLLPVLL 12
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DISULFID
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                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viruses, no RNA stage; Caudovirales; Siphoviridae.
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PubMed=1470232;
DOI=10.1128/JB.186.2.535-542.2004;
Streit W.R., Schmitz R.A., Perret X., Staehelin C., Deakin W.J.,
Raasch C., Lisesgang H., Broughton W.J.;
"An evolutionary hot spot: the pNGR234b replicon of Rhizobium sp
strain NGR234";
J. Bacteriol. 186:535-542(2004).
EMBL; AY316746; AAQ87226.1; -.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR011592; Surf4_rel.
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Jahamid megaplasmid 2.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                           Score 40; DB 1; Length 117;
Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 138;
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69.2%; Pred. No. 1.18+02;
Vienatches 3; Indels
By similarity.
By similarity.
CC -> SS (in Ref. 2).
7 19F969F94D58FA34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Origins of highly mosaic mycobacteriophage genomes.";

Cell 113:171-182(2003)

EMBL; AY12933; AAN12612.1; -

SEQUENCE 138 AA; 14405 MW; 120D21C12BBADAF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              138 AA.
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  54 99 BY
74 113 BY
53 54 CC
117 AA; 11425 MW;
                                                                                                                                58.8%;
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                                                                                                                                                                                                                                                                8 KLACAVLLCIVVAAP 22
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                                                                                                                                                                               9; Conservative
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les 9; Conservative
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                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=205872;
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Last sequence update)
Last annotation update)

Created) PRT;

153 AA

PRELIMINARY;

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MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398; Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boiseard P., Backer A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Manuty M., Kiss E., Lelaure V., Manuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Penard C., Thebault P., Vandenbol.M., Weidner S., Galibert F.; Sinorhizobium mailtori strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

EMBL; ALS91783; CAC41906.1; Complete proteome: Pytochetical protein.

SEQUENCE 153 AA; 15998 MW; 604679A394F98672 CRC64;
                                                                                                                Rhizobium mellioti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                     Hypothetical protein SMc02178.
ORFNames=SMc02178;
                                                     01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 61.5
hes 8; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                            NCBI_TaxID=382;
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MEDLINE=95291280; PubMed=7773253; DOI=10.1016/0965-1748(94)00056-N;
Krogh T.N., Roepstorff P., Andersen S.O., Hoejrup P.;
"Primary structure of proteins from the wing cuticle of the migratory locust, Locusta migratoria.";
Insect Biochem. Mol. Biol. 25:319-329(1995).
                                                                              Gaps
                                                                                                                                                                                                                     01-0CT-1989 (Rel. 12, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Cuticle protein 64 (LM-64) (LM-ARP 64).
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
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                                                  Query Match 58.8%; Score 40; DB 2; Length 138; Best Local Similarity 75.0%; Pred. No. 1.1e+02; Matches 9; Conservative 1; Mismatches 2; Indels
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HG -> PH (in Ref. 2).

A -> Y (in Ref. 2).

AAI -> LAL (in Ref. 2).

A -> Y (in Ref. 2).

A -> Y (in Ref. 2).

H -> Q (in Ref. 2).

W, OCI27C22F28E2941 CRC64;
ProDom; PD010195; Surf4 rel; 1.
Hypothetical protein; Plasmid.
SEQUENCE 138 AA; 14245 MW; C87156EDIEB080F7 CRC64;
                                                                                                                                                                                                 152 AA
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75 AALVLIPVLLGA 86
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Length 153;

58.8%; Score 40; DB 2; Length 153 61.5%; Pred. No. 1.2e+02; viewatches 2; Indels

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STRAIN-Dupont;

MEDLINE-21608550; PubMed=11743193; DOI=10.1126/science.1066804;

MOGULNE-21608550; PubMed=11743193; DOI=10.1126/science.1066804;

MOGULNE, Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liso L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley R., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Nester E.W.;

The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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SEQUENCE 158 AA; 17553 MW; 242AFA4D18DDF415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypotheical protein Atu1998.
                                                                                                                                                                                                                                                                                                                                                                   158 AA.
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PIR; A97600; A97600.
PIR; A12821; A12821.
3 AAAVLLPVLLAAP 15
                                                          PRELIMINARY,
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NCBI_TaxID=375;
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Local Similarity 71.4%;
hes 10; Conservative (
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                                                                                                                                                                                                      preliminary data.
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SEQUENCE FROM N.A.
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Q9HIX9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21608551; PubMed=11743194; DOI=10.1126/science.1066803; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Gielo C., Slater S.; "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CS8."; Science 294:2323-2328(2001).
                                                               Gaps
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                   AGR_C_3631p.
OrderedLocusNames=AGR_C_3631;
OrderedLocusNames=AGR_C_3631;
Bacbacterium tumefaciens (strain C58 / ATCC_33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium. NCBI_TaxID=176299;
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                Score 40; DB 2; Length 158;
Pred. No. 1.2e+02;
0; Mismatches 4; Indels
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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                58.8%;
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                                                                                                            3 AAAVLLPVLLAAP 15
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                Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity
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Name=NCU09978.1;
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STRAIN=OR74A;
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Q7CY40
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MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
RUEDD A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
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                                                                                                                                                                                              Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea, Buryarchaeota, Thermoplasmata, Thermoplasmatales,
Thermoplasmataceae, Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.8%; Score 40; DB 2; Length 168
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 4; Indels
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SEQUENCE 168 AA; 17345 MW; 9345611183ECA1D8 CRC64;
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EMBL; AL445066; CAC12322.1; -.

Interpro; IPR009058; Wing_hlx_DNa_bnd.

Complete protecome; Hypothetical protein.

SEQUENCE 252 AA; 27640 MW; BD2916EC4C4B9F06 CRC64;
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1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein 1197.
OrderedLocusNames=Tal197;
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Pred. No. 1.8e+02;
0; Mismatches 4;
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Query Match
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                      Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                           "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizoblum japonicum USDA110."; DNA Res. 9:189-197(2002). EMBL; AP005962; BAC52852.1; -.
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MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
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Enterobacteriaceae; Shigella.
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Submitted (MAR.2002) to the BMBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which preliminary data.
EMBL; AAABO1008880; EAA08668.1; -. SEQUENCE 297 AA; 30551 MW; 7D60098FFE259BBS CRC64;
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                                                                                                                                                                                                                                                                                Score 40; DB 2; Length 279;
Pred. No. 2e+02;
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                                                                                                                                                                                                                                     279 AA; 29666 MW; 27651945C0E13C39 CRC64;
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=agCG45893; ORFNames=ENSANGG0000017897;
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Shigella flexneri.
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                      MEDLINE=22484998; PubMed=12597275;
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174 KKAAKILGPLLLA 186
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115 AAILLPVIVGTP 126
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Best Local Similarity 58.3
Matches 7; Conservative
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SEQUENCE 279 AA:
  STRAIN=USDA110
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                                                                                                       Tabata S.;
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0083R77
AC 0083R7
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Q7QB91
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                                                                                      Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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57.1%; Pred. No. 2.1e+02;
ive 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome; Hypothetical protein.
SEQUENCE 390 AA; 41090 MW; 9598D66EEAEFD207 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.1.007-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE1001.
OrderedLocusNames=APE1001;
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                                                                                                                                                                                                                                                                                                                                                                              InterProj IPR000408; Reg chr_condens. PERM, Perm, Pronsel, Perm, Pronsel, Perm, 1, 1.
PRINTS; PR00183; ECCLIPORIN.
PRINTS; PR00182; ECCLIPORIN.
COMPLETE; PS00626; RCCI. 2; UNKNOWN_1.
COMPLETE PROFOCH: PORIN.
SEQUENCE 298 AA; 32637 MW; EE86B491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=99310339; PubMed=10382966;
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EMBL; AP000060; BAA79985.1; -.
PIR; A72698; A72698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desulfurococcaceae; Aeropyrum
NCBI_TaxID=56636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RKVLALLIPALLAA 16
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nes 8; Conservative
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180 AAKLLPLLAAAP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
    AE007984; AAK86294.1;
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SEQUENCE FROM N.A.
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Q70PA4
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"Genome sequence of the plant pathogen and biotechnology agent Science 294:2323-2328 (2001).
                                                                                                                                                                                                                                                                                                                                                                                        Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillett W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome of the natural genetic engineer Agrobacterium tumefaciens
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STRAIN=Dupont;
MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
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0
                                                                                                                                                                                                        Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Batceria, Proteobacteria, Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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SEQUENCE 431 AA; 47698 MW; 003ABCC90FE732F9 CRC64;
                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                  431 AA
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PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
                                                                                                                                                               Exopolysaccharide production protein.
Name=exoQ; OrderedLocusNames=Atu0481;
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                                                PRT;
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PIR; AF2635; AF2635.
PIR; E97417; E97417.
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                                                PRELIMINARY;
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                                                                                           01-JUN-2002
01-JUN-2002
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Q7D1D9;
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Matches
RESULT 40
Q8UI19
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Cystobacterineae, Cystobacteraceae, Melittangium.
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Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                      Length 435;
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ENGLY, AND 1994; AND 1994;
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EMBL. AJS57546; CAD89767.1; -.
HYpothetical protein.
SEQUENCE 450 AA; 49816 MW; 7243648A50D9BESC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                      58.8%;
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4 RRLSALLLPWLFAAP 18
                                                                                                                                                                                                                                                             Query Match
Query Match
Best Local Similarity 75.v.,
Best Local 9; Conservative
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OrderedLocusNames=SAV5036;
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Melittangium lichenicola.
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147 KASAVEAPVVMSAP 160

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NCBI_TaxID=9823;
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Q9XT90;
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SIGNAL
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                                                                             Ikeda H., Ishikawa J., Haramoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
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Nat. Biotechnol. 21:526-531(2003).
BMBL, APD05041; BAC72748.1;
GO: GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.
GO: GO:0009515; F:protein binding; IEA.
GO: GO:0009515; P:protein binding; IEA.
InterPro; IPR002502; Amidase_2.
InterPro; IPR006619; PGRP.
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MEDLINE=2296544; PubMed=14602910; DOI=10.1093/nar/gkg874;

Cerdeno-Tarraga A.-M.; Efstraction A., Dower L.G., Holden M.T.G.,

Ballen M.J., Bencley S.D., Besra G.S., Churcher C.M., James K.D.,

De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,

Hambin N., Holroyd S., Jagels K., Moule S., Quail M.A.,

Rabbinowitseh E., Rutherford K.M., Thomson N.R., Unwin L.,

Whitehead S., Barrell B.G., Parkhill J.;

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Nucleic Acids Res. 31:6516-6523(2003).

Nucleic Acids Res. 31:6516-6523(2003).

Nucleic Acids Res. 31:6516-6523(2003).

CO: GO: 0009959; F:phosphate acetyltransferase activity; IEA.

GO: GO: 0009959; F:phosphate acetyltransferase activity; IEA.

CO: GO: 0009959; F:phosphate acetylty; IEA.

CO: GO: 0009559; PTB. PTB.

InterPro: IPR002505; PTB. PTB.

InterPro: IPR002505; PTB. TIGN.

Acyltransferase; Complete protecome; Transferase.

CW Acyltransferase; Complete protecome; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 58.8%; Score 40; DB 2; Length 458; Local Similarity 61.5%; Pred. No. 3.1e+02; les 8; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 2; Length 483;
Pred. No. 3.3e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome, Hypothetical protein.
SEQUENCE 458 AA; 47722 MW; 02F837E43702989A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Phosphate acetyltransferase (EC 2.3.1.8).
Name=pta; OrderedLocusNames=DIP2055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                         STRAIN=MA-4680;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.8%;
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01510; Amidase 2; 1. SMART; SMO0701; PGRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium diphtheriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AAAVLLPVLLAAP 15
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14 AAALVLPLTLTAP 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q6NF46
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Matches
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2 KAAAVLLPVLLAAP 15

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"Matrix Biol. 17:501-511(1998).

"Matrix Biol. 17:501-511(1998).

"I FUNCTION: Seems to specifically activate progelatinase A. May thus trigger invasion by tumor cells by activating progelatinase A on the tumor cell surface (By similarity). May play a role in the biomineralization of enamel and dentin.

"CATALYTIC ACTIVITY: Endopeptidase activity. Activates progelatinase A by cleavage of the propeptide at 37-Asn-|-Leu-38.

"COPALYTIC ACTIVITY: Endopeptidase activity. Activates progelatinase A by cleavage of the propeptide at 37-Asn-|-Leu-42 and 38-Gin-|-Inta-355 in the aggrecan interglobular domain.

"COPACTOR: Binds 1 zinc ion per subunit, calcium (By similarity).

"SUBLIABLIAR DOCATION: Type I membrane procein (Potential).

"SUBLIABLIY: Belongs to the peptidase MIOA family.

"SIMILARITY: Contains 1 hemopexin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99095929; PubMed=9881602; DOI=10.1016/S0945-053X(98)90098-1;
Caron C., Xue J., Bartlett J.D.;
"Expression and localization of membrane type 1 matrix
                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00546; CYSTEINE SWITCH; 1.
PROSITE; PS00024; HEMOPEXIN, 1.
PROSITE; PS00142; ZIPP PROTEASE; 1.
Calcium; Hydrolase; MeTalloprotease; Signal; Transmembrane; Zinc;
                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Matrix metalloproteinase-14 precursor (EC 3.4.24.80) (MMP-14)
Membrane-type matrix metalloproteinase 1) (MT-MMP 1) (MTMMP1)
(Membrane-type-1 matrix metalloproteinase) (MT1-MMP).
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Matrix metalloproteinase-14.
Extracellular (Potential).
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   580 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR006026; Peptidase M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00045; Hemopexin; 4.
Pfam; PF00413; Peptidase_M10; 1.
Pfam; PF0393; Peptidase_M10, 1.
PRINTS; PR00138; MATRIXIN.
SMART; SM0120; HX; 4.
SMART; SM00225; ZNMC; 1.
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STANDARD;
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.

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Okada A., Bellocq J.P., Rouyer N., Chenard M.P., Rio M.C., Chambon P.,
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                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DF502B1; Q92678;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Matrix metalloproteinase-14 precursor (EC 3.4.24.80) (MMP-14)
(Membrane-type matrix metalloproteinase 1) (MT-MMP 1) (MTMMP1)
(Membrane-type-1 matrix metalloproteinase) (MT1-MMP) (MT1-MMP)
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MEDLINE=95237627; PubMed=7721107; DOI=10.1016/0378-1119(94)00637-8;
Takino T., Sato H., Yamamoto E., Seiki M.;
"Cloning of a human gene potentially encoding a novel matrix metalloproteinase having a C-terminal transmembrane domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "CDNA sequence and mRNA tissue distribution of a novel human matrix metalloproteinase with a potential transmembrane segment."; Eur. J. Biochem. 231:602-608(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Placenta;
MEDLINE=94286011; PubMed=8015608; DOI=10.1038/370061a0;
Sato H., Takino T., Okada Y., Cao J., Shinagawa A., Yamamoto E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A matrix metalloproteinase expressed on the surface of invasive
                                                                                                                                                                                                                                                                                                ô
                                                                                      (By similarity). (By similarity).
                                (By similarity).
                                                                                                                                                                                                                                  58.8%; Score 40; DB 1; Length 580; 90.0%; Pred. No. 3.9e+02;
                                                                                                                                                                                                                                  Zinc (catalytic) (By similar
By similarity.
Zinc (catalytic) (By similar
Zinc (catalytic) (By similar
By similarity.
W, B7B2C2C569A96CAC CRC64;
     Cysteine switch (Potential)
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Luo G.X., Reisfeld R.A., Strongin A.Y.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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Lohi J.L., Westermarck J., Kaehaeri V.M., Keski-Oja J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       582 AA.
                                                                                                                                                                                                                                                                                          1; Mismatches
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MEDLINE=95377289; PubMed=7649159;
                                                                                                                                                                            65934 MW;
                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    ||||:|||||
537 AAAVVLPVLL 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour cells.";
Nature 370:61-65(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                         580 AA;
                                                                                                                                                                                                                                                             Best Local Similarity
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PubMed-8804434;

PubMed-8804434;

Sato H., Kinoshita T., Takino T., Nakayama K., Seiki M.,

Sato H., Kinoshita T., Takino T., Nakayama K., Seiki M.,

Sato H., Kinoshita T., Takino T., Nakayama K., Seiki M.,

"Activation of a recombinant membrane type 1-matrix metalloproteinase

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or send an email to license@isb-sib.ch).
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R GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0004222; F:metalloendopeptidase activity; TAS.

GO; GO:0004220; F:metalloendopeptidase activity; TAS.

GO; GO:0006508; P:proteolysis and peptidolysis; TAS.

R InterPro; IPR000585; Hemopexin.

R InterPro; IPR000585; Pept_MZn_BS.

R InterPro; IPR006025; Pept_MZn_BS.

R InterPro; IPR006025; Pept_MZn_BS.

R InterPro; IPR00045; Hemopexin; 4.

R Pfam; PF000413; Peptidase_M10; 1.

R Pfam; PF000413; Peptidase_M10; 1.

R Pfam; PF00333; Peptidase_M10, 1.

R RNART; SM00120; HX; 4.

R SMART; SM00120; HX; 4.

R SMART; SM00120; HX; 4.

R PROSITE; PS00044; HEMOPEXIN; 1.

R PROSITE; PS00044; HEMOPEXIN; 1.

R PROSITE; PS00142; ZINC_PROTEASE; 1.

R PROSITE; PS00142; ZINC_PROTEASE; 1.

R PROSITE; PS00141; Transmembrane; Zinc; Zymogen.

T SIGNAL
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Cysteine switch (Potential).
Zinc (catalytic) (By similarity).
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Matrix metalloproteinase-14.
Extracellular (Potential).
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EMBL; X83535; CAA58519.1; --
EMBL; X40481; CAA8372.1; --
EMBL; U41078; AAA83770.1; --
EMBL; X90925; CAA62432.1; --
PIR; I38028; I38028.
PDB; 1BQQ; X-ray; M=114-287.
PDB; NHO.014; --
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MIM; 600754; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95224014; PubMed=7708715;
Okada A., Bellocg J.P., Rouyer N., Chenard M.P., Rio M.C., Chambon P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells of human colon, breast, and head and neck carcinomas."; Proc. Natl. Acad. Sci. U.S.A. 92:2730-2734(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus
Zinc (catalytic) (By similarity).
By similarity.
K -> E (in Ref. 2, 4, 5 and 6).
S -> P (in Ref. 6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.8%; Score 40; DB 1; Length 582; 90.0%; Pred. No. 3.9e+02;
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                       65883 MW; EFCEDCE6A41116F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Mmp14; Synonyms=Mtmmp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 90.0
Matches 9; Conservative
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539 AAAVVLPVLL 548
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                                                                                                                                                     STRAIN=CD-1; TISSUE-Kidney;
MEDLINE=98311877; PubMed=9648071;
Ota K., Stetler-Stevenson W.G., Yang Q., Kumar A., Wada J.,
Kashihara N., Waliner E.I., Kanwar Y.S.;
"Cloning of murine membrane-type-1-matrix metalloproteinase (MT-1-MMP)
and its metanephric developmental regulation with respect to MMP-2 and
its inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99449306; PubMed=10520996; DOI=10.1016/S0092-8674(00)80064-1;
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Biol. Chem. 272:25511-25517(1997).
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IPR006025; Pept_M Zn_BS.
IPR006026; Peptidase_M.
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EMBL; AF022444; AAB86602.1; JOINED.
EMBL; AF022425; AAB86602.1; JOINED.
EMBL; AF022426; AAB86602.1; JOINED.
EMBL; AF022427; AAB86602.1; JOINED.
EMBL; AF022428; AAB86602.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kidney Int. 54:131-142(1998).
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EMBL; AF022430; AAB86602.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00045; Hemopexin; 4
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EMBL; U54984; AAB51753.1;
HSSP; P50281; 1BQQ.
MEROPS; M10.014; -.
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                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | RMBL; U83118; AAB41500.1; -...
| RMBL; U73940; AAD13803.1; -...
| RMSCPS; MO.014; -...
| RMSCPS; MO.014; -...
| R InterPro; IPR000585; Hemopexin.
| R InterPro; IPR001818; Pept Moa M12B. |
| InterPro; IPR006025; Pept Man B. |
| InterPro; IPR006025; Pept Man B. |
| R Pfam; PF00413; Peptidase M10; 1...
| Pfam; PF03933; Peptidase M10; 1...
| R Pfam; PF03933; Peptidase M10; 1...
| R RARP; SM00120; MA; A. |
| R RARP; SM00120; MA; A. |
| R ROSTIE; PS00024; FEWOPEXIN; 1...
| R ROSTIE; PS00024; CYSTEINE SWITCH; 1...
| R ROSTIE; PS00024; ZINC_PROTEASE; 1...
| R ROSTIE; PS000142; ZINC_PROTEASE; 1...
| R Calcium; Hydrolase; Metalloprotease; Signal; Transmembrane; Zinc; |
| R ROSTIE; PS00046; CYSTEINE SWITCH; 1...
| R ROSTIE; PS000142; ZINC_PROTEASE; 1...
| R ROSTIE; PS00142; ZINC_PROTEASE; 1...
            the tumor cell surface (By similarity).

-!- CATALYTIC ACTIVITY: Endopeptidase activity. Activates progelatinase A by cleavage of the propeptide at 37-Asn-|-Leu-38. Other bonds hydrolyzed include 35-GJy-|-Ile-36 in the propeptide of collagenase 3, and 341-Asn-|-Phe-342, 441-Asp-|-Leu-442 and 354-GIn-|-Thr-355 in the aggreean interglobular domain.
-!- COPACTOR: Binds 1 zinc ion per subunit, calclum (By similarity).
-!- SUBCELULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Belongs to the peptidase M10A family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   remogrant...txe.
Cysteine switch (Potential).
Zinc (catalytic) (By similarity).
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
By similarity.
0 -> K (in Ref. 2).
K -> N (in Ref. 2).
E -> D (in Ref. 2).
E -> D (in Ref. 2).
E -> D (in Ref. 2).
GQP -> RTT (in Ref. 2).
GQP -> RTT (in Ref. 2).
GLISTS -> RTT (in Ref. 2).
K -> N (in Ref. 2).
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Matrix metalloproteinase-14.
Extracellular (Potential).
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Seems to specifically activate progelatinase A. May thus
trigger invasion by tumor cells by activating progelatinase A on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential).

Hemopexin-like.

Cysteine switch (Potential).

Zinc (catalytic) (By similarity).

By similarity.

Zinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

By similarity.

P -> S (in Ref. 3).

R -> D (in Ref. 3).

N -> P (in Ref. 1).

N -> P (in Ref. 1).

N -> T (in Ref. 1).

PC -> CV (in Ref. 1).
Pfam; PF00413; Peptidase M10; 1.
Prints, PR0333; Peptidase M10, N; 1.
PRINTS; PR00133; MATRIXIN.
SMART; SM01235; ZnMc; 1.
SMART; SM00235; ZnMc; 1.
SMOSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Calcium; Collagen degradation; Extracellular matrix; Hydrolase; SIGNAL
SIGNAL
1. 20
Prential.
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095220; P79225;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Matrix metalloproteinase-14 precursor (EC 3.4.24.80) (MMP-14)
(Membrane-type matrix metalloproteinase 1) (MTMMP1)
(Membrane-type-1 matrix metalloproteinase) (MTI-MMP) (MTMMP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.8%; Score 40; DB 1; Length 582; llarity 90.0%; Pred. No. 3.9e+02; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  By similarity.
Matrix metalloproteinase-14.
Extracellular (Potential).
Potential.
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STRAIN=New Zealand white; TISSUE=Vascular smooth muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang H., Keiser J.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3AB355158D4DD175 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65935 MW;
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539 AAAVVLPVLL 548
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512
582 AA;
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                                                 Score 40; DB 1; Length 582; Pred. No. 3.9e+02; Mismatches 0; Indels
                          844624B0AF1B6812 CRC64;
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Extracellular (Potential).

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Search completed: June 2, 2005, 01:39:49
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                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=95224014; PubMed=7708715;
Okada A., Bellocg J.P., Rouyer N., Chenard M.P., Rio M.C., Chambon P.,
Basset P.;
                                                                                                                                                                                                                                      "Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells of human colon, breast, and head and neck carcinomas."; Proc. Natl. Acad. Sci. U.S.A. 92:2730-2734(1995).
                                                                                                                                        kattus norvegicus (kat).
Eukaryota, Metaza, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodenta, Sciurognathi, Muridae, Murinae, Rattus
                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
02-0CT-2004 (Rel. 45, Last annotation update)
Antix metalloproteinase-14 precursor (EC 3.4.24.80) (MMP-14)
(Membrane-type matrix metalloproteinase I) (MT-MMP I) (MTMMPI)
(Membrane-type-1 matrix metalloproteinase) (MTI-MMP) (MTIMMP) (MTIMMP)
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Calcium; Hydrolase; Metalloprotease; Signal; Transmembrane; Zinc; Zymogen.
Zymogen.
I 20 Potential.
PROPEP 21 111 Activation peptide.
CHAIN 112 582 Matrix metalloproteinase-14.
                    582 AA
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RGD, 620198; Mmp14.
InterPro; IPR000585; Hemopexin.
InterPro; IPR000585; Pept_MOA_M12B.
InterPro; IPR006025; Pept_MZB_BS.
InterPro; IPR006025; Pept_Idase_M.
Pfan, PF0040413; Peptidase_M.0; 1.
Pfan, PF00413; Peptidase_M.0; 1.
Pfan, PF003933; Peptidase_M.0; 1.
SWART; SM00120; HX, 4.
SWART; SM00120; HX, 4.
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                    PRT;
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                                                                                                                        Name=Mmp14; Synonyms=Mtmmp;
Rattus norvegicus (Rat).
                    STANDARD;
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                    MM14 RAT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                 Cycoplasmic (Potential).
Hemopexin-like.
Cysteplasmic (Potential).
Zinc (catalytic) (By similarity).
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Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
I -> M (in Ref. 2).
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Zhang B., Yan L., Moses M.A., Fang J., Miao H., Tsang P.
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF290429; AGG28170.1; -.
HSSP; PS0281; 1BQQ.
MEROPS; M10.014; -.
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Membrane-type matrix metalloprotease 1.
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PROSITE; PS00142; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Metalloprotease; Protease.
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Pfam; PF03933; Peptidase_M10_N; 1.
Pfam; PF00138; MARRIXIN.
SWART; SW00120; HX; 4.
SWART; SW00225; ZnMc; 1.
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The specification describes a lipid-nucleic acid complex, comprising a compacted nucleic acid, a polycation, a targeting factor and a lipid, but not a protamine. The targeting factor increases cellular bloavailability of the nucleic acid without interaction with a specific outer cell courface membrane receptor. The mean diameter of the complex is greater than 100 nm and less than 400 nm. The lipid-nucleic acid complex is cuseful for delivering a nucleic acid to a cell in vivo, e.g. for gene cuseful for delivering a nucleic acid to a cell in vivo, e.g. for gene cerosis factor alpha. The complex is useful for manufacturing a necrosis factor alpha. The complex is useful for manufacturing a medicament for treating or diagnosing a variety of diseases, conditions or syndromes such as cancer, bacterial, viral or parasitic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited genetic diseases). The present sequence represents a targeting factor for lipid-nucleic acid complexes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
                                                                                                                                                                                                                                                    Lipid-nucleic acid complex; polycation; targeting factor; gene therapy; cancer; infection; immune deficiency; gene defect; genetic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "S(galactose), cholesteryl-succinyl, DOPE-
succinyl, DSPE-PEG5K-succinyl, DMPE-PEG5K-succinyl, or
DSPE-PEG5K-succinyl attached"
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100.0%; Pred. No. 6.2e-05;
                                                                                                                                                                                        Amino acid sequence of targeting factor Gelan094
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                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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ABP70234 standard; peptide; 15 AA
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(EMER-) EMERALD GENE SYSTEMS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 AA;
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Modified-site
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Matches 15;
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Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition, useful for treating a pathological disease in an animal, comprises a translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a composition which comprises a translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment of at least 4 amino acids of the transport peptide. The composition is useful in treating a pathological disorder in an animal, as it protects an orally delivered active agent from enzymatic degradation in the gastrointestinal tract (GIT), and promotes absorption across epithelial cells lining the GIT. The present sequence is a polypeptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 68; DB 8; Length 15; 100.0%; Pred. No. 6.2e-05; ive 0; Mismatches 0; Indels
                                                             /note= "modified by epsilon-dansyl"
                                                                                                                                                                                                                                                                                                                                                                          Pinilla C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human membrane translocating peptide (MTLP) #2.
                                                                                                         /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                          Houghten R,
                    Location/Qualifiers
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                                                                                                                                                                                                                                          21-APR-2003; 2003WO-US012543
                                                                                                                                                                                                                                                                                     19-APR-2002; 2002US-00126845
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nes 15; Conservative
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                    Key
modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a lipid-nucleic acid complex, comprising a not a protesting factor and a lipid, but not a protesting factor and a lipid, but not a protesting factor increases cellular bioavailability of the nucleic acid without interaction with a specific outer cell surface membrane receptor. The mean diameter of the complex is greater than 100 nm and less than 400 nm. The lipid-nucleic acid complex is therapy. It reduces levels of inflammatory cytokines such as tumour necrosis factor-alpha. The complex is useful for manufacturing a nucleic acid to a cell in vivo, e.g. for gene therapy. It reduces levels of inflammatory cytokines such as tumour medicament for treating or diagnosing a variety of diseases, conditions or syndromes such as cancer, bacterial, viral or parasitic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
                                                                                                  Lipid-nucleic acid complex; polycation; targeting factor; gene therapy; cancer; infection; immune deficiency; gene defect; genetic disease; membrane translocating peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic diseases). The present sequence represents a membrane translocating peptide, which is used as the targeting factor in lipidnucleic acid complexes of the invention
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                                                         Amino acid sequence of membrane translocating peptide Elan094.
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                                                                                                                                                                                                                                                                                                                                                                                                                 TARGETED GENETICS CORP. EMERALD GENE SYSTEMS LTD
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Matches 15; Conservative
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Query Match

RESULT 3 ABG75426

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lipid, and does not comprise protamine or its salt.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
ADB88776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                      The sequence represents a human membrane translocated peptide (WTLP).

WILPS and their related fragments, morifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer lining the gastrointestinal tract), eithor the directly or from a pharmaceutically active agent loaded particle, into the dircularcy system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the intracellular gene delivery, as a rapid screening method for the cidentification of MTLP which retain the functional activity of a MTLP, as a cell-based screen for assaying the functional activity of a MTLP and characterising the properties of a MTLP for diagnosis of a pathological disorder (by administration of a MTLP-active agent complex or or MTLP-active particle complex comprising a diagnostic agent) and for preventing or treating a pathological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                           Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipid-nucleic acid complex; polycation; targeting factor; gene therapy; cancer; infection; immune deficiency; gene defect; genetic disease; membrane translocating peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of membrane translocating peptide ZElan094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 68; DB 4; L4
100.0%; Pred. No. 6.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'mahony DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP70215 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TARG-) TARGETED GENETICS CORP.
(EMER-) EMERALD GENE SYSTEMS LTD.
                                                                                                                                                                                                                                                                               Claim 2; Page 11; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cudmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-2002; 2002WO-US013609.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KKAAAVLLPVLLAAP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                              O'mahony DJ, Lambkin IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
(LAMB/) LAMBKIN I J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-183837/18.
                                                                                         WPI; 2001-300212/31
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                                                                                                                  N-PSDB; AAS00627
                                                                                                                                                                                                                                    the peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200288318-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP70215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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PRO SECTION OF SECTION
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The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mRNM is greater than in a non-Peyer's patch cell. The preferred protein of the
                                                                                                         compacted nucleic acid, a polycation, a targeting factor and a lipid, but not a protamine. The targeting factor increases cellular bioavailability of the nucleic acid without interaction with a specific outer cell surface membrane receptor. The mean diameter of the complex is greater than 100 nm and less than 400 nm. The lipid-nucleic acid complex is useful for delivering a nucleic acid to a cell in vivo, e.g. for gene therapy. It reduces levels of inflammatory cytokines such as tumour necrosis factor-alpha. The complex is useful for manufacturing a medicament for treating or diagnosing a variety of diseases, conditions or syndromes such as cancer, bacterial, viral or parasitic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited genetic diseases). The present sequence represents a membrane translocating peptide, which is used as the targeting factor in lipid-nucleic acid complexes of the invention
                                                                                 complex, comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peyer's patch cell; non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 68; DB 6; Length 16; 100.0%; Pred. No. 6.6e-05; ive 0; Mismatches 0; Indels
                                                                             specification describes a lipid-nucleic acid
Disclosure, Page 10, 259pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 51; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Membrane translocating peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB88776 standard; peptide; 16 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane translocating peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KKAAAVLLPVLLAAP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2003 (first entry)
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Byrne D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OMAH/) O'MAHONY D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-229409/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 AA;
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localise the MTLP in a cell or tissue sample. MTLPs and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer lining the gastrointestinal tract), either directly of from a pharmaceutically active agent loaded particle, into the circulatory system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the identification of MTLPs which retain the functional activity of a full-length MTLP, as a cell-based screen for assaying the functional activity of a full-length MTLP, and characterising the properties of a MTLP, for diagnosis of a pathological disorder (by administration of a MTLP, for diagnosis of a pathological disorder (by administration of a MTLP, agent complex or MTLP-active particle complex comprising a diagnostic agent) and for preventing or

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Gaps

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Score 68; DB 4; Length 19; Pred. No. 8e-05; ; Mismatches 0; Indels

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15; Conservative

Local Similarity

Query Match Matches 1 KKAAAVLLPVLLAAP 15

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100.0%;

treating a pathological disorder

Sequence 19 AA;

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invention is a transcription factor or a protein that activates a transcription factor selected from Jun-B, c-jun related TF, Jun-D, STAT 3 sugnal transducer and activator of transcription 3, Nfkappakoby; Tf pl05 subunit, S-myc proto-oncogene, myc related, Nm3-M2, uncleoside diphosphate kinase B, metastasis reducing protein, and C-est-I proto-oncogene, and p54. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein CDS precursor, HSP 84, and Ca2+ dependent phospholipase A2 precursor and the mRNA is for a protein selected from the group. The method is useful for increasing or decreasing the level of a protein in a Peyer's patch cell, particularly in increasing antigen or vaccine delivery to M cells. The method may also be used to enhance transport of a drug through the gastrointestinal tract (GIT). This sequence represents a membrane translocating peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system; targeting peptide.
                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                               Score 68; DB 7; Length 16;
Pred. No. 6.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "N-terminus has a dansyl group"
                                                                                                                                                                                                                                100.0%; Scor.
100.0%; Pred. No. b...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human targeting peptide sequence #1.
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                                                                                                                                                                                                                                                                                                                                                                                                        AAU00655 standard, peptide; 19 AA.
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                                                                                                                                                                                                                                                                                                                        KKAAAVLLPVLLAAP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                            Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-300212/31.
                                                                                                                                                                                                                     Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1999;
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invention.
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Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a human membrane translocated peptide (MTLP). MTLPs and their related fragments, motifs, derivatives and analogues are used for enhanding uptake of a pharmacoutically active agent into a cell, into or out of an intracellular compartment and across a cell layer example, an epithelial cell layer lining the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle, into the circulatory system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the identification of MTLPs which retain the functional activity of a full-
                                                                                                                                                                                                     Human membrane translocating peptide (MTLP) #3.
                                                                                                AAU00634 standard, peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 11; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2000; 2000WO-IB001491.
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       15
                                                                                                                                                                   07-SEP-2001 (first entry)
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1 KKAAAVLLPVLLAAP
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(LAMB/) LAMBKIN I J.
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                                                                                                                                                                                                                                                                                                                           WO200127154-A2.
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                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          19-APR-2001.
                                                                                                                                  AAU00634;
                                                                                AAU00634
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Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic

The sequence represents a human targeting peptide which is used to identify the presence of a human membrane translocated peptide (MTLP) and quantify the amount, to bind the MTLP to the surface of a particle, or to

Example 1; Page 22; 42pp; English.

of the peptides.

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Composition, useful for treating a pathological disease in an animal, comprises a translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment of at least 4 amino acids of the transport peptide. The composition is useful in treating a pathological disorder in an animal, as it protects an orally delivered active agent from enzymatic degradation in the gastrointestinal tract (GIT), and promoces absorption across epithelial ciells lining the GIT. The present sequence is a polypeptide used in the exemplification of the invention
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a composition which comprises a
                                                                                                             o;
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                                                                   Length 19,
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                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "modified by epsilon-dansyl"
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100.0%; Pred. No. 8e-05;
iive 0; Mismatches 0;
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                                                                                       8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Membrane translocating peptide; transmembrane enzymatic degradation; gastrointestinal tract.
                                                                   100.0%; Score 68; DB
100.0%; Pred. No. 8e-
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                              ABG75428 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Membrane translocating peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Fr.
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hes 15; Conservative
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                             Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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length MTLP, as a cell-based screen for assaying the functional activity of a MTLP and characterising the properties of a MTLP, for diagnosis of pathological disorder (by administration of a MTLP-active agent complex or MTLP-active particle complex comprising a diagnostic agent) and for preventing or treating a pathological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peyer's patch cell; non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell; membrane translocating peptide.
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                                                                                                                                                                            100.0%; Score 68; DB 4; Length 19; 100.0%; Pred. No. 8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                 ADB88777 standard; peptide; 19 AA.
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Best Local Similarity 100.0
Matches 15; Conservative
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                                                                                                                                  Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
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ADB88777
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ABP70216;

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Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic
                                                               Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a human membrane translocated peptide (MTLP). MTLPs and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer for example, an epithelial cell layer lining the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle, into the circulatory system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the identification of MTLPs which retain the functional activity of a full-length MTLP, as a cell-based screen for assaying the functional activity of a MTLP and characterising the properties of a MTLP. for diagnosis of a pathological disorder (by administration of a MTLP-active agent complex or MTLP-active particle complex compressing a diagnostic agent) and for preventing or treating a pathological disorder.
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                    Human membrane translocating peptide (MTLP) #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 11; 42pp; English.
                                                                                                                                                                                                                                                                                         27-SEP-2000; 2000WO-IB001491.
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Matches 15; Conservative
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                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes a lipid-nucleic acid complex, comprising a compacted nucleic acid, a polycation, a targeting factor and a lipid, but not a protamine. The targeting factor increases cellular bioavailability of the nucleic acid without interaction with a specific outer cell surface membrane receptor. The mean diameter of the complex is greater than 100 nm and less than 400 nm. The lipid-nucleic acid complex is useful for delivering a nucleic acid to a cell in vivo, e.g. for gene therapy. It reduces levels of inflammatory cytokines such as tumour necrosis factor-alpha. The complex is useful for manufacturing a medicament for treating or diagnosing a variety of diseases, conditions or syndromes such as cancer, bacterial, viral or parasitic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited genetic diseases). The present sequence represents a membrane translocating peptide, which is used as the targeting factor in lipid-nucleic acid complexes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
                                                                                                                                                                                                                                                                               Lipid-nucleic acid complex; polycation; targeting factor; gene therapy; cancer; infection; immune deficiency; gene defect; genetic disease;
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                                                                                      ABP70216 standard; peptide; 20 AA.
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(EMER-) EMERALD GENE SYSTEMS LTD.
                                                                                                                                                                                                                                                                                                           cancer; infection; immune defic
membrane translocating peptide.
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Matches 15; Conserv
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Gaps

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Unidentified

07-SEP-2001 (first entry)

AAU00632;

RESULT 12 AAU00632

Query Match

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WO2003004646-A2

16-JAN-2003

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Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic
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99US-0156246P.
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                                                                                                                        Lambkin IJ;
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                                                (OMAH/) O'MAHONY D J.
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                                                                                                                                                                      WPI; 2001-300212/31.
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                                                                     (LAMB/) LAMBKIN I
                                                                                                                                                                                             N-PSDB; AAS00629
                                                                                                                                                                                                                                                                                                                        of the peptides.
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27-SEP-1999;
                                                                                                                        O'mahony DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mRNA is greater than in a non-Peyer's patch cell. The preferred protein of the invention is a transcription factor or a protein that activates a transcription factor or a protein that activates a transcription factor of transcription 3. NKappabagis, Tf plos channel transducer and activator of transcription 3. NKappabagis, Tf plos cubunt, S-myc proto-oncogene, myc related, Nm23-M2, nucleoside diphosphate kinase B, metastasis reducing protein, and C-est-I proto-oncogene, and p54. The preferred upregulated protein of the invention is elected from clusterin, T-cell surface glycoprotein CDs precursor, HSP elected from the group. The method is useful for increasing or derreasing protein selected from the group. The method is useful for increasing or decreasing antigen or vaccine delivery to M cells. The method may also be used to enhance transport of a drug through the gastrointestinal tract (CIT). This sequence represents a membrane translocating peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
                                                                                                                                                                                                                                                                                                                                                                    Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 68; DB 7; Length 21;
; Pred. No. 9e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human membrane translocating peptide (MTLP) #4.
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AAU00635 standard; peptide; 16 AA.

RESULT 14

07-SEP-2001 (first entry)

AAU00635;

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27-SEP-2000; 2000WO-IB001491.

WO200127154-A2 Homo sapiens

100.0%;

Ouery Match
Best Local Similarity luv...
15, Conservative

Sequence 21 AA;

nvention

Example 6; Page 51; 147pp; English.

factor.

Brayden D;

Byrne D,

O' mahony DJ,

WPI; 2003-229409/22.

(OMAH/) O'MAHONY D J.

04-APR-2001; 2001US-0281387P, 02-JUL-2001; 2001US-0302591P, 04-APR-2002; 2002WO-IB003866

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Gaps

Fri

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The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mRNA is greater than in a non-Peyer's patch cell. The preferred protein of the transcription factor or a protein that activates a cranscription factor selected from Jun-B. c-jun related Try Jun-D, STAR 3 signal transducer and activator of transcription 3, Nfkappa&bgr; Tf plo5 subunit, S-myc proto-oncogene, myc related, Nm23-M2, nucleoside chiposphate kinase B, metestasis reducing protein, and C-est-I proto-oncogene, and p54. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein CD5 precursor, HSP 84, and Ca2+ dependent phospholipase A2 precursor and the mRNA is for a protein selected from the group. The method is useful for increasing or decreasing the level of a protein in a Peyer's patch cell, particularly in increasing antigen or vaccine delivery to M cells. The method may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                             used to enhance transport of a drug through the gastrointestinal tract [T]. This sequence represents a membrane translocating peptide of the
              Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 7; Length 16; Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane translocating peptide; transmembrane transport; enzymatic degradation; gastrointestinal tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "modified by epsilon-dansyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pinilla C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houghten R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                Example 6; Page 51; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG75429 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Membrane translocating peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-2003; 2003WO-US012543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-APR-2002; 2002US-00126845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KKAAAVLLPVLLAAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKCAAVLLPVLLAAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 93.3
les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'mahony DJ, Lambkin I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-034528/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003089458-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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Matches
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                    an
                                                                                                                               translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment of at least 4 amino acids of the transport peptide. The composition is useful in treating a pathological disorder in an animal, as it protects an orally delivered active agent from enzymatic degradation in the gastrointestinal tract (GIT), and promotes absorption across epithelial cells lining the GIT. The present sequence is a polypeptide used in the exemplification of the invention
Composition, useful for treating a pathological disease in an animal, comprises a transport peptide, ar extended peptide comprising the transport peptide or a transport-active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition, useful for treating a pathological disease in an animal, comprises a transport peptide, an extended peptide comprising the transport peptide or a transport-active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a composition which comprises a translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment of at least 4 amino acide of the transport peptide. The composition is useful in treating a pathological disorder in an animal, as it protects
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                   present invention relates to a composition which comprises a
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                      ; DB 8; Lems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houghten R, Pinilla C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membrane translocating peptide; transmembrane enzymatic degradation; gastrointestinal tract.
                                                                                                                                                                                                                                                                                                                  Score 64; DB E
Pred. No. 0.000
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG75427 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Membrane translocating peptide #2.
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                                                                                  Claim 1; Page 24; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1, Page 24; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2003; 2003WO-US012543.
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-2002; 2002US-00126845
                                                                                                                                                                                                                                                                                                                                                                                     1 KKAAAVLLPVLLAAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lambkin I,
                                                                                                                                                                                                                                                                                                                                                                                                                    1 KKCAAVLLPVLLAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-034528/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SARL-) SARLAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003089458-A2
                                                                                                                                                                                                                                                                                   Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-2003
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Gaps

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Indels

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Mismatches

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14;

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1 KKAAAVLLPVLLAAP Conservative

KKKAAVLLPVLLAAP

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Lipid-nucleic acid complex; polycation; targeting factor; gene therapy; cancer; infection; immune deficiency; gene defect; genetic disease.
                                                                                                                                                                                                        Amino acid sequence of targeting factor Elan094G.
                                                                                                                           ABP70233 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TARG-) TARGETED GENETICS CORP.
(EMER-) EMERALD GENE SYSTEMS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2002; 2002WO-US013609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-2001; 2001US-0287786P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-183837/18.
                                                                                                                                                                                                                                                                                                                                                                                       WO200288318-A2
                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                07-APR-2003
                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harvie P,
                                                                                                                                                      ABP70233;
     Matches
                                                                                               RESULT 19
                                                                                                              ABP7023
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                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a lipid-nucleic acid complex, comprising a compacted nucleic acid, a polyation, a targeting factor and a lipid, but not a protamine. The targeting factor increases cellular bioavailability of the nucleic acid without interaction with a specific outer cell surface membrane receptor. The mean diameter of the complex is greater than 100 nm and less than 400 nm. The lipid-nucleic acid complex is useful for delivering a nucleic acid to a cell in vivo, e.g. for gene therapy. It reduces levels of inflammatory cytokines such as tumour necrosis factor-alpha. The complex is useful for manufacturing a medicament for trading or diagnosing a variety of diseases, conditions or syndromes such as cancer, bacterial, viral or parasitic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited genetic diseases). The present sequence represents a membrane translocating peptide, which is used as the targeting factor in lipid-nucleic acid complexes of the invention
                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
                                                                                                                                                                                                                                                                                                                                                             complex; polycation; targeting factor; gene therapy; immune deficiency; gene defect; genetic disease;
an orally delivered active agent from enzymatic degradation in the gastrointestinal tract (GIT), and promotes absorption across epithelial cells lining the GIT. The present sequence is a polypeptide used in the exemplification of the invention
                                                                                                                             Gaps
                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of membrane translocating peptide ZElan207.
                                                                                                  Length 14;
                                                                                                                           Indels
                                                                                               DB 8; Len
0.00042;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'mahony DJ;
                                                                                                92.6%; Score 63; DB 100.0%; Pred. No. 0.0; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 10; 259pp; English
                                                                                                                                                                                                                                                    ABP70217 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TARGETED GENETICS CORP. EMERALD GENE SYSTEMS LTD.
                                                                                                                                                                                                                                                                                                                                                                                       membrane translocating peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cudmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-2001; 2001US-0287786P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-2002; 2002WO-US013609
                                                                                                                                                      2 KAAAVLLPVLLAAP 15
                                                                                                                                                                                 1 KAAAVLLPVLLAAP 14
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                            Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-183837/18.
                                                                                                                                                                                                                                                                                                                                                              Lipid-nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harvie P, Paul R,
                                                                                                                                                                                                                                                                                                                                                                           cancer; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä
                                                                        Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200288318-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                          07-APR-2003
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                                                                                                                                                                                                                                                                               ABP70217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EMER-)
                                                                                                                                                                                                                          RESULT 18
                                                                                                                                                                                                                                       ABP70217
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O'mahony

Cudmore S,

Paul R,

"galactose attached"

/note=

'note= "Des-Pro attached"

Location/Qualifiers

(first entry)

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The specification describes a lipid-nucleic acid complex, comprising a compacted nucleic acid, a polycation, a targeting factor and a lipid, but not a protamine. The targeting factor increases cellular bioavailability of the nucleic acid without interaction with a specific outer cell card without interaction with a specific outer cell card explain the mucleic acid without interaction with a specific outer cell card explain the manual less than 400 nm. The lipid-nucleic acid complex is greater therapy. It reduces levels of inflammatory cytokines such as tumour cherapy. It reduces levels of inflammatory cytokines such as tumour cardicament for treating or inflammatory cytokines such as tumour corrosis factor-alpha. The complex is useful for manufacturing a concerplation or syndromes such as cancer, bacterial, viral or parasitic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited genetic diseases). The present sequence represents a targeting factor for lipid-nucleic acid complexes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 0.001;
ive 0; Mismatches 0; Indels
                                                                                                                                                                         Disclosure; Page 42; 259pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
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Matches
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Length 15;

Score 63; DB 6; Pred. No. 0.00046;

92.6%;

Query Match Best Local Similarity

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The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 127.
                                                                                                                                                                                                                                                                                                                                                                                        Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signal sequence MST (membrane-translocating
C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (fibroblast growth factor) signal sequence MST (membrane sequence) cell-penetrating polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cch 85.3%; Score 58; DB 8; I sal Similarity 100.0%; Pred. No. 0.0049; 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 225; 626pp; English.
                                                                                                                                                                                                                                                                                                                             Borrello MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK50915 standard; peptide; 21 AA.
                                                                                                                                                                                                            10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
                                                                                                                                                                              10-JUN-2003; 2003WO-US018252.
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                                                                                                                                                                                                                                                                           (VACC-) VACCINEX INC. (UYRP ) UNIV ROCHESTER.
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Best Local Similarity
Matches 13; Conserv
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                                                                                  Unidentified.
                                                                 Homo sapiens
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Unidentified
                                                                                                                                              18-DEC-2003,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating cequence) cell-penetrating polypeptide of the invention.
                                                                                                                                                          Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 123.
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                                                                                                                                                                                        C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 223; 626pp; English.
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                                                            ADK50911 standard; peptide; 21 AA.
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11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
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                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                          Homo sapiens.
Unidentified.
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Best Local S
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The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
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Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
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                                                                                                                                                                                                                                                                                                              ch 85.3%; Score 58; DB 8; Length 33; I Similarity 100.0%; Pred. No. 0.0081; 13; Conservative 0; Mismatches 0; Indels
                                                    Disclosure; Page 224; 626pp; English.
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23-APR-2003; 2003US-0464650P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 Sequence 33 AA;
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                                                                                                                                                                                                           Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
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                  10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
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11-DEC-2002; 2002US-0432241P.
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                                                                                      (VACC-) VACCINEX INC. (UYRP ) UNIV ROCHESTER.
                                                                                                                                          Zauderer M, Evans EE,
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Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 AA;
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ADK50916
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ADK50920

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New peptidomimetic compounds are tumor cell replication inhibitors useful to treat tumors or oncological disorders of e.g. breast, kidney, mouth, larynx, esophagus, stomach, testis, cervix, head, neck, colon, ovary, lung, bladder and skin.
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                                                                                                                                                                                                                                                                   peptidomimetic; Cytostatic; Tumour; Apoptosis; oncological disorder.
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86.7%; Pred. No. 0.0062;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                            Peptide comprising a membrane translocating sequence #2.
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                                                                                                     ADR40510 standard; peptide; 18 AA.
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    21 AAAVLLPVLLAAP 33
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Best Local Similarity 86.7
Matches 13; Conservative
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Modified-site
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                                                               RESULT 26
ADR40510
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carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
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100.0%; Pred. No. 0.0
iive 0; Mismatches
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11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
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                                                                                                                                                                                                                                 21 AAAVLLPVLLAAP 33
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                 13; Conservative
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                                                                                                                      Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                Seguence 33 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                            ADK50920;
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The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
                                                         Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB 8; Length 21;
Pred. No. 0.0073;
0; Mismatches 2; Indels
                                                                                                                          Disclosure; Page 203; 626pp; English.
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11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 AA;
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Unidentified.
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                                                                                                                                                                                                                                                                                                                            New peptidomimetic compounds are tumor cell replication inhibitors useful to treat tumors or oncological disorders of e.g. breast, kidney, mouth, larynx, esophagus, stomach, testis, cervix, head, neck, colon, ovary, lung, bladder and skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to peptidomimetic compounds and their salts. The compound is useful in the treatment of a tumour or an oncological disorder (breast, kidney, mouth, larynx, oesophagus, stomach, testis, cervix, head, neck, colon, ovary, lung, bladder, skin, muscle, panortess, prostate, bone, eye, blood cells or brain cancers) in a human or animal. The present sequence represents is a peptide comprising a membrane translocating sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 43.
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                                                                                                                                                                                                                                                         Hamilton AD;
/note= "phosphorylated"
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11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
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Best Local Similarity
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                                        WO2004073650-A2
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antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
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                                                                                                                                                   Gaps
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                                                                                                                     83.8%; Score 57; DB 8; Length 33; 86.7%; Pred. No. 0.012; 2; Indels ive 0; Mismatches 2; Indels
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Pred. No. 0.011;
2; Mismatches 1; Indels
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11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
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                                                                                                                                  Best Local Similarity 86.7
Matches 13, Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                              Sequence 33 AA;
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The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
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11-DEC-2002; 2002US-043224IP.
23-APR-2003; 2003US-0464650P.
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1 KKAAAVLLPVLLAAP
                                  Zauderer M, Evans EE,
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Unidentified
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Gaps

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The specification describes a fusion protein for regulating normal or infected cell function, comprising an antibody conjugated to a peptide having immunostimulatory, membrane transport, and homophilic activities. The antibody is immunospecific for a signaling protein internal cell consisting of caspases, kinases or phospharases, an immature viral protein, a cell-surface or intracellular tumour antigen, a nuclear or nucleolar protein participating in regulation of DNA synthesis and gene expression, or a cytoskeletal protein participating in cell proliferation or cytostasis. The peptide portion of the fusion protein is preferably a membrane transporter peptide that is endogenous to Kaposi fibroblast factor, TAT peptides of HIV-1, antennapedia homeodomain-derived peptide, herpes virus protein VP22, or transportan peptide. Fusion protein of the preventing human diseases, e.g., Alzheimer's diseases, Huntington's disease or Parkinson's disease. CG membrane transporter peptide which is derived from Kaposi fibroblast con proteins of the content of the factor. The peptide is used to produce fusion proteins of the
                                                                                                                                                                                                                 caspase; kinase; phosphatase; viral protein; tumour antigen; protein; nuclear protein; nucleolar protein; DNA synthesis; cytoskeletal protein; cell proliferation; cytostasis; membrane transporter peptide; Kaposi fibroblast factor; TAT peptide; HIV-1; antennapedia homeodomain; herpes virus protein VP22; transportan peptide; Albheimer's disease; Huntington's disease; Parkinson's disease; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New compound for regulating normal or infected cell function comprising an antibody conjugated to a membrane transporter peptide, useful in preparing a composition for treating or preventing human diseases, e.g.
                                                                                                                                                                       immunostimulatory; membrane transport; homophilic; signaling protein;
                                                                                        Membrane transporter peptide from Kaposi fibroblast growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morgan AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 8; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INNE-) INNEXUS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAR-2004; 2004WO-US006911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-2003; 2003US-0451980P.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMP-) IMMPHERON INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-653567/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004078146-A2.
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02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kohler H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nvention.
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Gaps ; Length 17; 1; Indels DB 8; 0.013; Score 55; DB 8 Pred. No. 0.013 1; Mismatches Query Match
Best Local Similarity 85.7%;
Watches 12; Conservative ò

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EGAAVLLPVLLAAP 16 2 KAAAVLLPVLLAAP 15

ADR88404 standard; peptide; 17 AA. ADR88404; RESULT 33

16-DEC-2004 (first entry)

Mouse MTS membrane translocation peptide

tryptophan photoactivation; malignancy; cancer; tumour; auto-immune disorder; transplantation rejection; Alzheimer's disease; neurodegenerative condition; membrane translocation peptide. Mouse; antibody; autophilic; MTS; T15; dimerisation; apoptosis;

Mus sp.

US2004185039-A1

23-SEP-2004.

29-AUG-2003; 2003US-00652864.

30-AUG-2002; 2002US-0407421P.

(KOHL/) KOHLER H. (MORG/) MORGAN A C.

Kohler H, Morgan AC;

Treating patient suffering from debilitating or life threatening disease such as malignancy, by administering autophilic antibody capable of binding to cellular receptors to promote target cell apoptosis, to WPI; 2004-676149/66

Example 2; SEQ ID NO 2; 9pp; English.

patient

The invention relates to treating a patient suffering from a debilitating or life threatening disease, involving administring at least one sutophilic antibody to the patient in an amount effective to alleviate symptoms of the disease. An autophilic antibody is a non-covalent, dimerisation. Also included by the attachment of a peptide which induces dimerisation. Also included are potentiating apoptosis of selected cells of antibody period administering to the patient first autophilic antibody period administering to the patient of treat autophilic antibody period administering techniques (where the autophilic antibody by charging administering the autophilic antibody by contains a T15 autophilic peptide sequence appearing an autophilic antibody by contains a T15 autophilic peptide sequence that further potentiates the ability of the modified out autophilic oppide sequence that further potentiates the ability of the modified auto antibody to crosslink once bound to a target antigen relative to the unmodified auto antibody, formulating an autophilic antibody composition of salt concentrations of to.8M or more, low levels of sodium dodecyl or peptide sequence or miligate dimerisation in solution (comprising addition of salt concentrations of the antibody to ataget antibody considered or modifications of the antibody of antibody to severe or modifications of the antibody of antipody and antibody confider (supplied say of an antibody and antibody and antibody confiders (involving administering the autophilic antibody to severe combined immuno deficiency (SCID) or nude mice having human tumour combined immuno deficiency (SCID) or nude mice having human tumour combined immuno deficiency (SCID) or nude mice having one or more conservative subshilic coupling peptides seach having one or more conservative subshility peptides are conjugated to different selfenting from a debilitating or a template peptide, and comparing self-binding properies egence of template peptide, or these new conservative peptides are conjugated to entry into the target cell

Sequence 17 AA

RESULT 35

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a novel membrane-translocating peptide sequence (MTS). The invention relates to the use of the MTS peptides for pereing fusion proteins which can be used for the production of polypeptides of interest such as Schistosoma japonicum glutathion of transferase, an adenovirus E3 19K protein or a mammalian p53 protein. Fusions of the peptides can also be used for inducing an immune response in a mammal using e.g. a viral polypeptide such as hepatitis B surface antigen. They can also be used for protecting a subject from an infectious agent using a polypeptide that inhibits reproduction of the infectious agent such as a protease inhibitor. They can also be used for treating cancer using a polypeptide thus suppressor such as p53 protein or a polypeptide inhibitor of B61-2. The methods can be used for treating canine, feline and bovine diseases and also for studying intracellular
                                                                                                                                                                                                                                                                                                                    Membrane-translocating peptide sequence; MTS; fusion protein; production; Schistosoma japonicum; glutathione S transferase; adenovirus; mammal; p53; immune response; hepatitis B virus; surface antigen; canine; feline; protease inhibitor; cancer; tumor suppressor; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides containing a membrane-translocating sequence used to develop
                                      Gaps
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 Score 55; DB 8; Length 17;
Pred. No. 0.013;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                     Membrane-translocating peptide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              products for use in, e.g. vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 66; 85pp; English.
                                                                                                                                                                                  AAY44160 standard; protein; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           којав М,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0080083P.
98US-00186170.
Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                    EGAAVLLPVLLAAP 16
                                                                   2 KAAAVLLPVLLAAP 15
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Local 12; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Donahue JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-610819/52.
N-PSDB; AAZ28749.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9949879-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1998;
04-NOV-1998;
                                                                                                                                                                                                                                                    01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                   AAY44160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin Y,
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Membrane translocating peptide; MTLP; human; intracellular gene delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a polypeptide comprising at least two peptide monomers, in which each peptide monomer comprises an amino acid sequence which serves as a nuclear localisation sequence (NLS) or an amino acid sequence which serves as a protein transduction domain (PTD) in eukaryotic cells. The polypeptide of the invention is used for transferring a molecule into eukaryotic cells. The use of a polypeptide comprising NLS or PTD drastically increases the efficiency of the transfer of attached molecules, preferably negatively charged molecules into the nucleus or cytoplasm of a eukaryotic cell. The present sequence is hydrophobic PTD which include the sequence of transportan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides comprising at least two monomers which comprise a nuclear localization sequence and protein transduction domain, respectively useful for transferring nucleic acid molecules into eukaryotic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.4%; Score 54; DB 4; Length 12;
100.0%; Pred. No. 0.013;
tive 0; Mismatches 0; Indels
                                                                                                                                          Peptide monomer; nuclear localisation sequence; NLS;
                                                                                                                                                         protein transduction domain; PTD; molecule transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human membrane translocating peptide (MTLP) #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                Rudolph CM, Plank C;
                                                                                                           Hydrophobic protein transduction domain #8.
                AAE02980 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU00644 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3, Page 32, 68pp; English.
                                                                                                                                                                                                                                                                                     23-NOV-2000; 2000WO-EP011690
                                                                                                                                                                                                                                                                                                                     99EP-00123423
                                                                            10-AUG-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenecker J, Ritter W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AAVLLPVLLAAP 15
                                                                                                                                                                                                                                                                                                                                                    ROSENECKER J.
                                                                                                                                                                                                                                                                                                                                                                                (RUDO/) RUDOLPH C M. (PLAN/) PLANK C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-367696/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   RITTER W.
                                                                                                                                                                                                                        WO200138547-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                     24-NOV-1999;
                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                      31-MAY-2001.
                                              AAE02980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU00644;
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ID AAUC
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AC AAUC
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DT 07-8
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AAE02980
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Gaps

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4 AAVLLPVLLAAP 15

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The invention relates to a composition (I) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or antibody. Also included are (I) a vaccine comprising (I). CPP associated with an antigen, and a pharmaceutically acceptable carrier and (2) preparing a composition for a disease, by providing (I) and CPP associated with an antigen for disease, and introducing the antigens associated with an antigen for disease, and introducing the antigens are, for example, tumour antigen derived epitopes recognised by tumour infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I or II. The composition is useful for enhancing immunity in an animal to a disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal, such that following comprises both CD4+ and CD8+ T cells. It is also useful for treating a disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, accomer, cervical cancer, bladder cancer and pancreatic cancer). The animal is further subjected to a cancer reatment including surgery, radiation, chemotherapy or gene therapy. The administration of (I), cancer is a concer treatment. The present sequence is cell penetrating peptide of the cancer treatment. The present sequence is cell penetrating peptide of
                                                                                                                                                                                                                                                                                                                                   Novel composition for treating a disease in an animal, comprises an immune effector cell and cell penetrating peptide associated with an antigen or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Membrane translocation signal; signal sequence based peptide I; red blood cell vehicle; polypeptide delivery; Grb2; SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.4%; Score 54; DB 5; Length 12; 100.0%; Pred. No. 0.013; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grb2 SH2 domain derived signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 10; 61pp; English.
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                                                                                                                                                                                               (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU78350 standard; peptide; 12
                                                                                               15-FEB-2002; 2002WO-US005212.
                                                                                                                                                15-FEB-2001; 2001US-0268687P.
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                                                                                                                                                                                                                                                                                               WPI; 2002-627577/67.
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les 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 AA;
WO200264057-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-2002
                                           22-AUG-2002.
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                                                                                                                                                                                                                                                Wang R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compositions for enhancing uptake of e.g. drugs or DNA across a cell
membrane, comprise membrane translocating peptides having specific amino
acid sequences or a derivative, fragment, motif, analog or peptidomimetic
of the peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a human membrane translocated peptide (MTLP). MTLPs and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer lining the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle, into the circulatory system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the indentification of MTLPs which retain the functional activity of a full-length MTLP, as a cell-based screen for assaying the functional activity of a MTLP and characterising the properties of a MTLP, for diagnosis of a phenlogical disorder (by administration of a MTLP-active agent complex arms.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or MTLP-active particle complex comprising a diagnostic agent) and for preventing or treating a pathological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell penetrating peptide; cancer; tumour; melanoma; thymoma; lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia; Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer; kidney cancer; adenocarcinoma; breast cancer; prostate cancer; ovarian cancer; pancreatic cancer; vaccine; dendritic cell; tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
epithelial cell layer; gastrointestinal tract; circulatory system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 11; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell penetrating peptide CPP1.
                                                                                                                                                                                               27-SEP-2000; 2000WO-IB001491
                                                                                                                                                                                                                                                99US-0156246P
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                                                                                                                                                                                                                                                                                                                                                                          O'mahony DJ, Lambkin IJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OMAH/) O'MAHONY D J.
                                                                                                                                                                                                                                                                                                                         LAMBKIN I J.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-300212/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AASO0638
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                                                                                             WO200127154-A2.
                                                                                                                                                                                                                                                27-SEP-1999;
                                                 Homo sapiens.
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dysfunctions of the gastrointestinal tract or liver, comprises cystic fibrosis transmembrane conductance regulator and a membrane translocation sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention discloses a method for preparing a delivery vehicle for delivering an agent to a target site in a vertebrate. The method comprises loading a cell with an agent-membrane translocation sequence (MTS) conjugate, which contains a membrane translocation sequence enabling the agent to crose the plasma membrane of a cell. Also disclosed is a pharmaceutical composition comprising a red blood cell for delivery
                                                                                                                                            The invention relates to a novel fusion protein comprising a cystic fibrosis transmembrane conductance regulator (CFTR) and a membrane translocation sequence (WTS). The sequence represents the membrane translocation sequence. The fusion protein of the invention has gastrointestinal, respiratory, and hepatotropic activity. The protein is taken up by affected cells and thereby used for treating cystic fibrosis or dysfunctions of the gastrointestinal tract or liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preparing a red blood cell vehicle suitable for delivering an agent to target site in a vertebrate due to loading the red blood cell with an
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Pred. No. 0.013;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                               79.4%; Scor.
100.0%; Pre
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                                                                                                       Claim 3; Page 15; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG75508 standard; peptide; 12
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09-AUG-2000; 2000WO-GB003556.
22-DBC-2000; 2000US-00748063.
22-DBC-2000; 2000US-00748789.
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nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                 Sequence 12 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an agent-MTS (membrane translocation sequence) conjugate. The red blood cells produced may be used in the preparation of a medicament for delivery of an agent to or at a target site and of one or more agents to a vertebrate. The agent is actively released from the red blood cell vehicle by application of a stimulus to disrupt the red blood cell vehicle. This sequence represents signal sequence derived from the Grb2 SH2 domain, one of the membrane translocation peptides tested in the
                                                                                                                                                                                                                                                                                                                                            Preparing a red blood cell vehicle suitable for delivering an agent to target site in a vertebrate due to loading the red blood cell with an agent-membrane translocation sequence.
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                                                                           24-JUL-2000; 2000WO-GB002848.
09-AUC-2000; 2000WO-GB003056.
01-FEB-2001; 2001WO-GB00417.
16-FEB-2001; 2001US-00785802.
                                24-JUL-2001; 2001WO-GB003327.
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                                                                                                                                                                                                                                                                                                 WPI; 2002-280593/32.
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                                                                                                                                                                                                 (GEND-) GENDEL LTD
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Best Local S
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Matches
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of an agent to a vertebrate, the red blood cell comprising the novel agent-MTS conjugate and a method of immunisation of an animal with an antigen. The method is useful for preparing delivery vehicles, particularly a red blood cell, for the intracellular delivery of a therapeutic agent to a target site. The method is particularly useful for selectively releasing the agent-MTS conjugate at a target cell, and for selectively releasing the agent by the cells at target site. The preferred MTS sequences are from HIV-1 trans-activating protein (Tat), Drosophila Antennapedia homeodomain protein (Antp-HD), Harpes Simplex-1 virus VP22 protein (HSV-VP22), a signal-sequence-based peptide and a Tranportan and Amphiphilc model peptide. The sequence presenced is the signal-sequence based peptide III, which is derived from the Grbz SH2
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Grb2; SH2 domain; membrane translocation.
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                                                                                                                                                                                                                                                                                                                                                 79.4%; Score 54; DB 5; Length 12; 100.0%; Pred. No. 0.013; ive 0; Mismatches 0; Indels
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16-FEB-2001; 2001US-0269528P
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les 12; Conservative
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                                                                                                                                                                                                                                                                    (not defined) domain
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for delivering one or more agents to a vertebrate and for treating or preventing a disease. The method is useful for delivering agents such as those useful for imaging of tissues in vivo or ex vivo, preferably for delivering an agent to a subcellular on a subcellular and a subcellular a su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virucide; cytostatic; vaccine; intercellular transport; antigenic; immune response; cytotoxic T lymphocyte; tumour; cancer; pcDNA3-E7/MTS; chronic viral infection; veterinary herpesvirus infection; pseudorabies; equine herpesvirus; bovine herpesvirus; Marek's disease virus; chicken; fowl; animal retroviral disease; rabies.
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                                                                                                                                                                                                                                                                                                                                    79.4%; Score 54; DB 5; Length 12; 100.0%; Pred. No. 0.013; ive 0; Mismatches 0; Indels
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15-FEB-2001; 2001US-0268575P.
04-APR-2001; 2001US-0281004P.
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Matches 12, Conservative
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                                                                                                                                                                                                                                                                        Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200209645-A2
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                                                                                                                                                                                                          translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU77231;
                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 42
      88888888888
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Peyer's patch cell; non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell; membrane translocating peptide.

04-APR-2002; 2002WO-IB003866. 04-APR-2001; 2001US-0281387P.

WO2003004646-A2.

16-JAN-2003.

Unidentified.

O'mahony DJ, Byrne D, (OMAH/) O'MAHONY D J.

Membrane translocating peptide #13.

04-DEC-2003 (first entry)

ADB88787;

ADB88787 standard; peptide; 12 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     one transport agent region and an active agent region. The transport agent region is able to facilitate the uptake of the active agent region. The transport into a cell. The active agent region is an active therapeutic agent region able to facilitate axon growth and an analogue. The drug delivery construct is useful for suppressing the inhibition of neuronal axon growth, facilitating axon growth, treating nerve injury, treating ischammic damage related to stroke injury. The drug delivery construct and the drug conjugate are useful for the manufacture of a pharmaceutical composition for treating nerve injury. The invention is useful in gene therapy. The present sequence is transport peptide used in the invention
acid sequence represents the peptide used in the methods of the invention for the generation of pcDNA3-E7/MTS expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a new drug delivery construct comprises at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New drug delivery construct comprising a transport and active agent region, useful for the manufacture of a pharmaceutical composition for treating nerve injury.
                                                                                                                                                                                                                                                                                                                                                                                                           Drug delivery construct; axon growth; nerve injury; ischaemic damage; stroke injury; gene therapy; neuroleptic; neuroprotective.
                                                                                                                     Gaps
                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.4%; Score 54; DB 6; Length 12; 100.0%; Pred. No. 0.013; tive 0; Mismatches 0; Indels
                                                                                  DB 5; Length 12; 0.013; hes 0; Indels
                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Transport peptide used in the invention.
                                                                                  Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 52; 188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOA-) BIOAXONE THERAPEUTIQUE INC
                                                                                                                                                                                                                                                                       AAE32065 standard; peptide; 12 AA.
                                                                                  79.4%; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-APR-2002; 2002WO-CA000480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-2001; 2001CA-02342970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-2001; 2001CA-02362004.
15-JAN-2002; 2002CA-02367636.
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                    12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                     4 AAVLLPVLLAAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-092963/08.
                                                                                                Similarity
                                                   Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200283179-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mckerracher L;
                                                                                                                                                                                                                                                                                                                                          24-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-2002;
                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                         AAE32065;
                                                                                                                                                                                                                                        RESULT 43
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The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mRNA is greater than in a non-Peyer's patch cell. The preferred protein of the invention is a transcription factor or a protein that activates a transcription factor or a protein that activates a transcription factor or a protein that activates a transcription factor selected from Jun-B, c-jun related TF, Jun-D, STAT 3 caignal transducer and activator of transcription 3, Nfkappa&bgr; Tf plos subunit, S-myc proto-oncogene, myc related, Nm3-M2, nucleoside ciphosphate kinase B, metastasis reducing protein, and C-est-I proto-oncogene, and p54. The preferred upregulated protein, of the invention is selected from clusterin T-cell surface glycoprotein CDS precursor, HSP 84, and Ca2+ dependent phospholipase A2 precursor and the mRNA is for a protein selected from the group. The method is useful for increasing or decreasing the level of a protein in a Peyer's patch cell, particularly in increasing antigen or vaccine delivery to M cells. The method may also be used to enhance transport of a drug through the gastrointestinal tract (GIT). This sequence represents a membrane translocating peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Pred. No. 0.013;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 51; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC22455 standard; peptide; 12 AA.
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100.0%; Fi
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nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-229409/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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ID ADC2
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Gaps

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4 AAVLLPVLLAAP 15

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us-10-764-235-2.rag

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nuclear localisation sequence; NLS; protein purification tagged sequence; gene delivery; kaposi's sarcoma-associated herpesvirus; FGF signal sequence; membrane fusion sequence.
                                                                                                                                             fusion protein; cold shock domain; membrane translocation sequence; CspA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion protein comprising a cold shock domain, and a membrane translocation sequence, useful for delivering DNAs and RNAs to in vivo cells for gene delivery.
                                                                                                                                                                 CspB; CspC; CspD; rpl Sl binding domain; eukaryotic Y-box protein; DNA binding protein B, DBBB; DBPA; RFR-1; mRNP3; mRNP4; FRG Y1; nuclease-sensitive element binding protein 1; NSEP 1; DNA condensation domain; DNA binding domain; SPKR;
                                                                                             Kaposi FGF signal membrane fusion sequence seq id 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; SEQ ID NO 19; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAY-2002; 2002US-00144549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-2002; 2002US-00144549
                                               26-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                Human herpesvirus 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-901590/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HWUP/) HWU P L.
                                                                                                                                                                                                                                                                                                                                                                                                                US2003211590-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-2003.
ADG28018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hwu PL;
The present invention describes a recombinant fusion protein (I) for detecting binding of a molecule of interest. (I) comprises: (a) a detection domain, (b) a first localisation domain, the first constituting the molecule of interest. The detecting domain, the first constituting the recombinant fusion protein for the molecule of interest are operably linked. The binding domain for the molecule of interest are operably linked. The binding domain for the molecule of interest is separated from the first localisation domain by 0 constituting the molecule of interest is separated from the first localisation domain by 0 constituting the molecule of interest both do not occur in a single non-recombinant protein with the same spacing as in the recombinant fusion protein with the same spacing as in the recombinant fusion protein with the same spacing as in the recombinant fusion protein with the same spacing as in the recombinant fusion protein.

(2) a recombinant expression vector comprising the nucleic acid control sequences operably linked to the recombinant the recombinant control sequences operably linked to the recombinant fusion protein.

(2) a recombinant action call encoding the recombinant fusion protein of interest; and (5) a method for identifying compounds that alter the binding of the molecule of interest. The recombinant fusion protein is useful for detecting binding of a molecule of interest. The recombinant fusion of fusion protein and enables the monitoring of biochemical events in live, inteat the process of interest is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant fusion protein comprising detection and first localization domains and a binding domain for the molecule of interest, useful for detecting binding of a molecule of interest.
                                                                                                                                     recombinant fusion protein; fusion protein; binding; detection; localisation domain; binding domain; subcellular compartment localisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.4%; Score 54; DB 7; Length 12; 100.0%; Pred. No. 0.013; ive 0; Mismatches 0; Indels
                                                                                             Protein-derived transport peptide SEQ ID NO:304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 304; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen Y;
                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-2002; 2002WO-US024572
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-2001; 2001US-0309395P
13-DEC-2001; 2001US-0341589P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.v.
The 12; Conservative
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bright G, Premkumar DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CELL-) CELLÒMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-248174/24.
                                                                                                                                                                                                                                                                                          WO2003012068-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 AA;
                                             18-DEC-2003
                                                                                                                                                                                                                                                                                                                                         13-FEB-2003
                                                                                                                                                                                                                                          Synthetic.
ADC22455,
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molecule into cells or mucles, comprising a cold shock domain, its homologue and functional derivative, and a membrane translocation sequence or its functional derivative, and a membrane translocation sequence or its functional derivative, and a membrane translocation sequence or its functional depty septides and/or derivatives. The functional comprises a cold shock domain, eukaryotic Y-box proteins, DNA Cobb protein is modified by inserting into the cold shock protein is modified by inserting into the cold shock protein is modified by inserting into the cold shock protein is selected from DNA condensation domain. The DNA condensation domain is selected from DNA condensation or binding domain is selected from DNA condensation domain. The CNA condensation or binding domain is selected from DNA condensation domain. The DNA condensation domain (SPRR) 3-4 and the positive charge nuclear localisation sequences (MIS+). The membrane fusion sequence is protein transduction domain (PPD) or membrane fusion sequence selected from HA, GST, and His6 tag. The fusion protein is useful for delivering nucleic acids to an embryo or cells for gene delivery, or for delivering nucleic acids to an embryo or to a living animal for the production of transgenic animal. This is the amino acid sequence of a membrane fusion sequence derived from Kaposi's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
The invention describes a fusion protein for delivery of a desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB 7; Length 12, Pred, No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sarcoma-associated herpesvirus FGF signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.4%; Scor.
100.0%; Pred. No. vo....
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH76185 standard; peptide; 12 AA.
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Best Local Similarity 100.0v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12 AA;
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ID ADH7
XX
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Gaps

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ADG28018 standard; peptide; 12 AA.

RESULT 46 ADG28018

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fusion protein; cold shock domain; membrane translocation; gene therapy; transgenic; membrane fusion; MPS; Kaposi FGF signal.
                                                                                                                                                                                                                                                                                                                                                                                                            New fusion protein comprising a cold shock domain, and a membrane translocation sequence, useful for delivering DNAs and RNAs to in vivo cells for gene delivery.
                                                                               MPS (Kaposi FGF signal sequence) membrane fusion sequence peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; SEQ ID NO 17; 53pp; Japanese.
                                                                                                                                                                                                                                                                                                                 (GENE-) GENESHUTTLE BIOPHARM INC.
                                                                                                                                                                                                                                                      15-MAY-2002; 2002JP-00140441.
                                                                                                                                                                                                                                                                                     13-MAY-2002; 2002US-00144549.
                                               20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-901590/82.
                                                                                                                                                                                        JP2004035409-A.
                                                                                                                                                           Unidentified
                                                                                                                                                                                                                         05-PEB-2004.
                 ADL88654;
                                                                                                                                                                                                                                                                                                                                                 Hwu PL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel polypeptide comprising a heat shock protein 20-derived polypeptide. A polypeptide of the invention has cyfosteratic, antiarteriosclerocite, vasotropic, antianginal, cerebroprotective, antiarchythmic, antiatehmatic, gynaecological, cerebroprotective, antiarchythmic, antiatehmatic, gynaecological, hypotensive, antimigraine, tocolytic, and relaxant activity, and may act as a HRSP agonist or antagonist. The polypeptides, heat shock protein (HSP) 20, and methods are useful for treating or preventing a disorder, e.g. intimal hyperplasia, stenosis, restenosis, transplant vasculopathy, atherosclerosis, smooth muscle cell tumours such as leiomyosarcoma, or vasospasm, which is associated with angina, coronary vasospasm, britanetal's angina, coronary ischeamia, stroke, bradycardia, hypertension, pulmonary (lung) hypertension, asthma (bronchospasm), coronary pre-eclampsia/eclampsia/eclampsia/s Raynaud's phenomenon, haemolytic-uremia, non-occlusive mesenteric ischaemia, anal fissure, achalasia, impotence, migraine, or polypeptides and HSP 20 are also useful for inhibiting smooth muscle cell proliferation and/or migration. The present sequence represents a peptide used in a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New heat shock protein 20-derived polypeptides, useful for inhibiting, treating or preventing smooth muscle cell vasospasm or a disorder such as intimal hyperplasia, restenosis, atherosclerosis or smooth muscle cell
                                                                                                           antianginal; cerebroprotective; antiarrhythmic; antiasthmatic; gynaecological; hypotensive; antimigraine; tocolytic; relaxant; HSP; smooth muscle cell; smooth muscle cell; transduction domain.
                                                                                           shock protein 20; cytostatic; antiarteriosclerotic; vasotropic;
                                                              Transduction domain peptide of the invention SEQ ID NO:286.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Lokesh J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.4%; Score 54; DB 7; Length 12; 100.0%; Pred. No. 0.013; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Seal B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 29; SEQ ID NO 286; 194pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Panitch A,
                                                                                                                                                                                                                                                                 23-AUG-2002; 2002WO-US026918
                                                                                                                                                                                                                                                                                                  23-AUG-2001, 2001US-0314535P
                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Brophy C, Komalavilas P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                BROPHY C.
KOMALAVILAS P.
                                                                                                                                                                                                                                                                                                                              UNIV ARIZONA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-393248/37
                                                                                                                                                                                                                                                                                                                                                                             PANITCH A.
                                                                                                                                                                                                                                                                                                                                                                                                              LOKESH J.
                                                                                                                                                                                                     WO2003018758-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12 AA;
                               22-APR-2004
                                                                                                                                                                                                                                    06-MAR-2003
                                                                                                                                                                        Synthetic.
ADH76185,
                                                                                                                                                                                                                                                                                                                                                           (KOMA/)
(PANI/)
(SEAL/)
(LOKE/)
                                                                                                                                                                                                                                                                                                                               (UYAR-)
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The invention relates to a novel fusion protein for delivery of a desired molecule into cells or nuclei comprising a cold shock domain, its homologue and functional derivative and a membrane translocation sequence or its functionally equivalent peptides and/or derivatives. The fusion protein of the invention may be useful for delivering DNAs and RNAs to in vivo cells for gene therapy or for delivering nucleic acids to an embryo or to a living animal for the production of transgenic animals. The current sequence is that of a membrane fusion sequence peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein; site-specific DNA recombinase domain;
nuclear localisation signal; NLS; gene alteration; cell culture;
cellular uptake; functional biopolymer; Karposi fibroblast growth factor.
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel recombinase-related Karposi growth factor peptide SeqID18
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                     Length 12;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                   Score 54; DB 7; Ler
Pred. No. 0.013;
                                                                                                                                                                                                      79.4%; Scor.
100.0%; Prev
0; }
                                                                                                                                                                                                                                                                                                                                                                                                                      ADN60178 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                             4 AAVLLPVLLAAP 15
                                                                                                                                                                                                                                                                                                                              AAVLLPVLLAAP
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003076561-A2
                                                                                                                                                                                  Sequence 12 AA;
                                                                                                                                                                                                                         Me.
Local s..
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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Gaps

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ADL88654 standard; peptide; 12 AA.

RESULT 48 ADL88654 ID ADL88

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invention.
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                                                                                                                                                                                                                                This invention relates to a novel fusion protein comprising a site-specific DNA recombinase domain and a domain containing a modified nuclear localisation signal (NLS) of type one having 5-10 amino acid residues and containing at least 5 basic amino acid residues and containing at least 5 basic amino acid residues and no Proresidue. The fusion protein is useful for preparing an agent for inducing target gene alterations in living organisms or in cell cultures, where the living organisms or cells of the cell cultures carry at least one or more recognition sites for the site-specific DNA recombinase integrated in its genome. The modified NLS is useful for enhancing cellular uptake of functional biopolymers in living organisms or cell cultures. The present sequence is that of a Karposi fibroblast growth factor peptide invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytoplasmic transduction peptide; cell membrane transduction potential; cell membrane transduction; cytotoxic T lymphocyte; drug delivery system.
                                                                                                                                           New fusion protein comprising a site-specific DNA recombinase domain as domain containing a modified nuclear localization signal, useful for preparing an agent for inducing target gene alterations in living
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100.0%; Pred. No. 0.013;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                           Claim 7; SEQ ID NO 18; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic transduction peptide MTS
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                       09-MAR-2002; 2002EP-00005468.
13-MAR-2002; 2002US-0363797P.
06-MAR-2003; 2003WO-EP002280
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                                                                (ARTE-) ARTEMIS PHARM GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
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N-PSDB; ADG12915.
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The present invention describes a cytoplasmic transduction peptide which has cell membrane transduction potential, where a cell is treated with the cytoplasmic transduction peptide for a period of time and then treated with a protease, a cell membrane transduction by the cytoplasmic transduction peptide continues to occur, and the cytoplasmic transduction membrane for cell. Also described: (1) a mucleic acid molecule encoding the cytoplasmic transduction peptide (2) a cytoplasmic transduction system comprising the cytoplasmic transduction peptide and a biologically active molecule covalently linked to the peptide; and (3) a method for delivering the biologically active molecule into the cytoplasm of a cell. The cytoplasmic transduction peptide is useful in inducing cytotoxic T lymphocytes and a drug delivery system targeting cytoplasm. The present sequence is used in the exemplification of the present
New cytoplasmic transduction peptide having a characterized cell membrane in the transduction potential, useful for inducing cytotoxic {\tt T} lymphocytes and a drug delivery system targeting cytoplasm.
                                                                                                                                                                                                                                                                            Example 1; Page 21; 77pp; English.
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Sequence 12 AA;

Gaps ö 79.4%; Score 54; DB 8; Length 12; 100.0%; Pred. No. 0.013; ive 0; Mismatches 0; Indels 12; Conservative Local Similarity Query Match Matches

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Sequence 12, Appli Sequence 12, Appl Sequence 10, Appl Sequence 1, Appli Sequence 286, App Sequence 1, Appli Sequence 304, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	Sequence 1, Appl Sequence 1, Appl Sequence 102, Appl Sequence 19, Appl Sequence 2, Appl Sequence 1, Appli Sequence 1, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 1, Appli	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	58, App 65, App 110, App 110, App 24, App 112, App 24, App 82, App 9, App 19, App	Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 15, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl
295-081A-8 Sequence 1278-816-12 Sequence 1278-802A-10 Sequence 128-16-286-16-286 Sequence 126-956-286 Sequence 126-956-286 Sequence 126-956-286 Sequence 126-956-286 Sequence 126-956-156-14-14-14-14-14-14-14-14-14-14-14-14-14-	-126 845-72 Sequence 7-136-187-12 Sequence 7-136-187-10 Sequence 7-144-549-19 Sequence 7-144-285-1 Sequence 7-744-235-1 Sequence 7-751-380-8 Sequence 8-751-380-8 Sequence 8-751-381-1 Sequence 8-751-	-634-645-1 Sequence 17, 25-081A-9 Sequence 9, 2823-259-38 Sequence 38, 2823-259-38 Sequence 38, 2902-959-51 Sequence 17, 2955-656-1 Sequence 17, 2955-656-14 Sequence 17, 2955-656-14 Sequence 17, 2948-193-1 Sequence 7, 2956-255-256-255-256-256-256-256-256-256-2	955-656-7 255-656-7 255-656-7 255-656-10 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 255-656-110 2	19, Appl 19, Appl 10, Appl 10, Appl 10, Appl 10, Appl 10, Appl 103, Appl 115, Appl 115, Appl 115, Appl 115, Appl 115, Appl 115, Appl 116, Appl 116
7 17 US-10-795-081A-8 Sequence E 2 9 US-09-789-836-12 Sequence 12 2 US-09-785-802A-10 Sequence 12 13 US-10-116-288-1 Sequence 12 13 US-10-116-288-1 Sequence 2 14 US-10-255-1 Sequence 2 14 US-10-211-088-304 Sequence 2 14 US-10-211-088-304 Sequence 2 14 US-10-126-845-1 Sequence 2 15 US-10-126-85-1 Sequence 2 US-10-126-	2 14 US-10-126-845-72 Sequence 72 15 US-10-136-187-1 Sequence 73 US-10-136-275-10 Sequence 73 US-10-136-28-19 Sequence 72 15 US-10-361-208-473 Sequence 72 15 US-10-361-208-473 Sequence 72 15 US-10-764-235-1 Sequence 73 US-10-764-235-1 Sequence 73 US-10-764-235-1 Sequence 74 US-10-764-235-1 Sequence 75 US-10-764-235-1 Sequence 75 US-10-761-388-1 Sequence 75 US-10-761-381-1 Sequence 75 US-10-7	17 US-10-634-645-1 Sequence 17, US-10-634-645-1 Sequence 9, 217 US-10-823-259-38 Sequence 9, 217 US-10-823-259-38 Sequence 38, 217 US-10-823-254-38 Sequence 38, 217 US-10-955-656-1 Sequence 17, 217 US-10-955-656-1 Sequence 17, 217 US-10-955-656-14 Sequence 17, 217 US-10-955-656-14 Sequence 17, 217 US-10-955-656-14 Sequence 72, 217 US-10-948-193-1 Sequence 7, 314 US-10-126-845-7 Sequence 7, 315 US-10-126-845-7 Sequence 7, 316 US-10-126-845-7 Sequence 7, 316 US-10-16-275-95 Sequence 7, 316 US-10-275-95 Sequence 7, 316 US-10-275-95 Sequence 7, 316 US-10-275-95 Sequence 7	16 US-10-764-235-58 Sequence 58, App 4 17 US-10-955-656-5 Sequence 7, Appl 10 US-10-955-656-15 Sequence 110, App 11 US-10-955-656-110 Sequence 110, App 12 US-10-955-656-110 Sequence 110, App 14 US-10-126-845-24 Sequence 82, App 15 US-10-126-845-12 Sequence 12, App 17 US-10-955-656-24 Sequence 24, App 17 US-10-955-656-82 Sequence 24, App 17 US-10-955-656-82 Sequence 24, App 11 US-10-126-845-19 Sequence 92, Appl 11 US-10-126-845-19 Sequence 93, Appl 14 US-10-126-845-19 Sequence 19, Appl 14 US-10-116-288-9 Sequence 19, Appl 14 US-10-116-288-9 Sequence 19, Appl 15 US-10-116-288-9 Sequence 19, Appl 16 US-10-116-288-9 Sequence 19, Appl 17 US-10-116-288-9 Sequence 19, Appl 18 US-10-116-288-9 Sequence 19, Appl 19 US-10-126-845-17 Sequence 17, Appl	1 10 105-106-106-106-106-106-106-106-106-106-106
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	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 326, Appli Sequence 2, Appli
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276-272A-11 276-272A-12 276-272A-12 276-272A-12 276-272A-12 276-272A-12 276-272A-12 276-272A-12 276-272A-12 28-27-12 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-27-13 28-	116-78 Sequence 116-78 Sequence 116-78 Sequence 116-78 Sequence 116-78 Sequence 116-88-6 Sequence 116-88-6 Sequence 116-88-110 Sequence 116-25-110 Sequence 116-25-12 Sequence 116-25-12 Sequence 116-25-13 Sequence 116-27-111 Sequence 116-27-111 Sequence 116-27-111 Sequence 116-27-112 Sequence 116-27-113 Sequence 116-27-118 Sequence 116-27-118 Sequence 116-37-31-318 Sequence
16 US-10-953-264-26 Sequence 16 US-10-276-272A-1 Sequence 16 US-10-276-272A-1 Sequence 16 US-10-276-272A-2 Sequence 16 US-10-276-272A-2 Sequence 17 US-10-914-97-85 Sequence 18 US-10-126-845-7 Sequence 18 US-10-126-845-7 Sequence 19 US-10-126-845-7 Sequence 19 US-10-126-845-7 Sequence 17 US-10-126-845-8 Sequence 17 US-10-126-845-8 Sequence 17 US-10-126-845-8 Sequence 17 US-10-955-656-7 Sequence 17 US-10-955-656-7 Sequence 17 US-10-955-656-112 Sequence 18 US-10-449-831A-49 Sequence 19 US-10-449-831A-49 Sequence 19 US-10-255-674-196 Sequence 19 US-10-255-674-196 Sequence 19 US-10-255-674-196 Sequence 19 US-10-282-122A-70499 Sequence 19 US-10-282-122A-70499 Sequence 19 US-10-282-122A-70499 Sequence 19 US-10-282-122A-70499 Sequence 19 US-10-33-346-14 Sequence 19 US-10-33-346-14 Sequence 19 US-10-33-346-34 Sequence 19 US-1	17 US-110-839-10429 Sequence 18 US-10-1156-761-10429 Sequence 19 US-10-1156-761-10429 Sequence 19 US-10-1156-845-22 Sequence 19 US-10-126-845-22 Sequence 10 US-10-126-845-22 Sequence 11 US-10-555-656-80 Sequence 12 US-10-555-656-80 Sequence 13 US-10-555-656-80 Sequence 14 US-10-955-656-80 Sequence 15 US-10-955-656-80 Sequence 16 US-10-126-845-71 Sequence 17 US-10-955-656-80 Sequence 18 US-10-126-845-71 Sequence 19 US-10-126-845-11 Sequence 10 US-10-955-656-13 Sequence 11 US-10-955-656-13 Sequence 12 US-10-955-656-13 Sequence 13 US-10-955-656-13 Sequence 14 US-10-955-656-13 Sequence 15 US-10-955-656-13 Sequence 16 US-10-955-656-13 Sequence 17 US-10-955-656-13 Sequence 18 US-10-955-656-13 Sequence 19 US-10-955-656-13 Sequence 10 US-10-955-656-13 Sequence 11 US-10-955-656-13 Sequence 12 US-10-955-656-13 Sequence 13 US-10-955-656-13 Sequence 14 US-10-955-656-13 Sequence 15 US-10-955-656-13 Sequence 16 US-10-955-656-13 Sequence 17 US-10-955-656-13 Sequence 18 US-10-955-656-13 Sequence 19 US-10-955-956-959-959-959-959-959-959-959-959
US-10-953-264-26 US-10-276-272A-11 US-10-276-272A-2 US-10-276-272A-12 US-10-276-272A-2 US-10-276-272A-12 US-10-276-272A-12 US-10-276-272A-12 US-10-276-272A-12 US-10-276-272A-12 US-10-116-28B-3 US-10-116-28B-3 US-10-126-845-17 US-10-126-845-17 US-10-126-845-17 US-10-126-845-17 US-10-126-845-17 US-10-126-845-18 US-10-126-845-19 US-10-127-963-141-5 US-10-128-128-141-5 US-10-128-128-141-5 US-10-128-128-141-5 US-10-137-963-189076 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	335 17 US-10-10-329 US-38 Sequence 335 17 US-10-10-329 US-38 Sequence 8 13 US-10-1156-761-10429 Sequence 8 14 US-10-1156-845-80 Sequence 8 14 US-10-126-845-80 Sequence 8 15 US-10-126-845-80 Sequence 8 17 US-10-126-845-110 Sequence 8 17 US-10-95-656-80 Sequence 10 US-10-126-845-11 Sequence 10 US-10-126-845-11 Sequence 110 US-10-126-845-11 Sequence 1110 US-10-126-845-11 Sequence 1120 US-10-126-845-11 Sequence 1130 US-10-126-845-11 Sequence 1130 US-10-126-845-11 Sequence 1130 US-10-126-943-2205- Sequence 1131 US-10-126-943-2205- Sequence 1132 US-10-126-943-2205- Sequence 1133 US-10-126-943-2205- Sequence 1248 US-10-128-112A-63318 Sequence 125 US-10-282-122A-63318 Sequence
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14 US-10-127-825A-296 14 US-10-127-829A-296 14 US-10-127-835A-296 14 US-10-127-839A-296 14 US-10-127-931A-296	US-10-131-813A-29 US-10-131-818A-29 US-10-131-823A-29	US-10-131-824A-29 US-10-131-824A-29 US-10-131-830A-29	US-10-131-837A-29 US-10-137-872A-29	US-10-147-500-29	US-10-147-515-29	US-10-147-517-29 US-10-147-526-29	US-10-147-527-29	US-10-121-041-29 US-10-121-043-29	US-10-121-047-29	US-10-123-215-29	US-10-123-902-29 US-10-123-908-29	US-10-123-909-29	US-10-123-910-29	US-10-124-813-29 US-10-124-817-29	US-10-125-922-29	US-10-125-924-29	US-10-140-860-29	US-10-142-417-29	US-10-14/-519-29	US-10-152-395-29	US-10-189-123-56	US-10-125-926A-29	US-10-125-930A-2	US-10-12/-831A-29	US-10-127-838B-29	US-10-127-842A-29	US-10-127-843A-29	US-10-127-845A-29	US-10-127-848A-23	US-10-127-849A-29	US-10-127-850A-29	US-10-127-851A-29	02-10-120-084A-29	US-10-128-690A-29	4 US-10-128-691A-29	4 US-10-131-819A-29	4 US-10-131-829A-29	4 US-10-146-729-296	4 US-10-146-791-29	4 US-10-147-484-29	4 US-10-147-508-29	4 US-10-175-735-29	4 US-10-121-040-29	4 US-10-121-056-29 4 US-10-121-061-29	4 US-10-121-001-23	4 US-10-124-818-29	4 US-10-137-868-29	4 US-10-147-492-29	4 US-10-158-782-29	3-123-905-2 1-123-907-2	4 US-104-521-01-50
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907-925-2 Sequence 2, 2902-692-2 Sequence 2, 903-520-2 Sequence 2, 905-056-2 Sequence 2, 909-064-2 Sequence 2, 909-053-2 Sequence 2, 909-053-2	9-905-381-2 Sequence 2, 9-904-485-2 Sequence 2, 9-904-485-2	9-905-048-2 Sequence 2, 9-905-088-2 Sequence 2, 9-907-575-2 Sequence 2,	9-905-075-2 Sequence 2, 9-902-759-2	9-902-634-2 Sequence 2,	9-907-979-2 Sequence 2,	7-902-615-2 9-903-925-2 Sequence 2,	9-906-760A-2 Sequence 2,	3-903-823-2 Sequence 2, 9-907-652-2 Sequence 2,	9-902-572A-2 Sequence 2,	9-902-979-2 Sequence 2,	9-905-123-2 9-906-815A-2 Sequence 2,	9-905-449-2 Sequence 2,	3-903-806-2 Sequence 2,	9-904-992-2 9-904-838-2 Seguence 2,	9-906-777-2 Sequence 2,	9-903-603A-2 Sequence 2,	9-904-532-2 Sequence 2,	9-904-766-2 Seguence 2,	3-904-920A-2 3-904-877A-2 Sequence 2	9-903-562-2 Sequence 2,	9-906-618-2 Sequence 2,	9-907-728-2 Sequence 2,	9-904-805-2 -004-030%-7	3-904-938A-2 3-906-7023-2	9-908-576-2 Sequence 2,	0-028-072-296 Seguence 29	0-140-808-296 Sequence 29	0-121-049-296 Sequence 29	7-123-904-290 Sequence 23	0-175-746-296 Sequence 29	0-176-918-296 Sequence 29	0-176-921-296 Sequence 29	J-13/-865-296 Sequence 23	0-142-431-296 Semience 29	0-143-114-296 Sequence 29	3-142-419-296 Sequence 29	J-123-262-296 Sequence 23	0-121-050-296 Sequence 29	0-141-755-296 Sequence 29	0-143-032-296 Sequence 29	J-123-108-296 Sequence 29	0-123-261-296 Sequence 29	0-140-921-296 Sequence 29	0-140-928-296 Sequence 29	7-121-043-296 Sequence 23	0-123-903-296 Sequence 29	3-124-819-296 Sequence 29	0-124-822-296 Sequence 29	0-140-925-296 Sequence 28	0-160-498-296 Sequence 29	J-124-824-296 sequence 25
10 US-09-907-925-2 Sequence 2, 10 US-09-902-692-2 Sequence 2, 10 US-09-903-520-2 Sequence 2, 10 US-09-905-056-2 Sequence 2, 10 US-09-905-056-2 Sequence 2, 10 US-09-905-055-3-2 Sequence 2, 10 US-09-904-553-2	10 US-09-905-381-2 Sequence 2, 10 US-09-904-485-2 Sequence 2, 10 IIS-09-904-485-3	10 US-09-905-088-2 Sequence 2, 10 US-09-907-575-2 Sequence 2,	10 US-09-905-075-2 Sequence 2, 10 US-09-902-759-2 Sequence 2,	10 US-09-902-634-2 Sequence 2,	10 US-09-907-979-2 Sequence 2,	10 US-09-902-615-2 Sequence 2, 10 US-09-903-925-2	10 US-09-906-760A-2 Sequence 2,	10 US-09-903-823-2 Sequence 2, 10 US-09-907-652-2	10 US-09-902-572A-2 Sequence 2,	10 US-09-902-979-2 Sequence 2,	10 US-09-905-123-2 Sequence 2,	10 US-09-905-449-2 Sequence 2,	10 US-09-903-806-2 Sequence 2,	10 US-09-904-992-2 Seguence 2,	10 US-09-906-777-2 Sequence 2,	10 US-09-903-603A-2 Seguence 2,	10 US-09-904-532-2 Sequence 2,	10 US-09-904-766-2 Sequence 2,	10 US-US-904-904-520A-2	10 US-09-903-562-2 Sequence 2,	10 US-09-906-618-2 Sequence 2,	10 US-09-907-728-2 Sequence 2,	10 US-09-904-805-2 Sequence 2,	10 US-US-904-938A-2 Sequence 2,	11 US-09-908-576-2 Sequence 2,	14 US-10-028-072-296 Seguence 29	14 US-10-140-808-296 Seguence 29	14 US-10-121-049-296 Sequence 29	14 US-10-123-904-296 Sequence 23	14 US-10-175-746-296 Sequence 25	14 US-10-176-918-296 Sequence 29	14 US-10-176-921-296 Sequence 29	14 US-IV-I3/-865-296 Sequence 25	14 US-10-142-431-296 Sequence 29	14 US-10-143-114-296 Sequence 29	14 US-10-142-419-296 Sequence 29	14 US-10-123-262-296 Sequence 23	14 US-10-121-050-296 Sequence 29	14 US-10-141-755-296 Sequence 29	14 US-10-143-032-296 Sequence 29	14 US-10-123-236-296 Sequence 23	14 US-10-123-261-296 Sequence 29	14 US-10-140-921-296 Sequence 29	14 US-10-140-928-296 Sequence 29	14 US-10-121-045-296 Sequence 29	14 US-10-123-903-296 Sequence 29	14 US-10-124-819-296 Sequence 29	14 US-10-124-822-296 Sequence 29	14 US-10-140-925-296 Sequence 29	14 US-10-160-498-296 Seguence 25	14 US-10-124-824-296 Sequence 23
0 US-09-907-925-2 Sequence 2, 0 US-09-902-692-2 Sequence 2, 0 US-09-903-520-2 Sequence 2, 0 US-09-905-056-2 Sequence 2, 0 US-09-905-056-2 Sequence 2, 0 US-09-905-055-2 Sequence 2, 0 US-09-904-53-2 Sequence 2, 0 US-09-904-53-2	10 US-09-905-381-2 Sequence 2, 10 US-09-904-485-2 Sequence 2, 10 IIS-09-904-485-3	10 US-09-905-088-2 Sequence 2, 10 US-09-907-575-2 Sequence 2,	10 US-09-905-075-2 Sequence 2, 10 US-09-902-759-2 Sequence 2,	10 US-09-902-634-2 Sequence 2,	10 US-09-907-979-2 Sequence 2,	10 US-09-902-615-2 Sequence 2, 10 US-09-903-925-2	10 US-09-906-760A-2 Sequence 2,	10 US-09-903-823-2 Sequence 2, 10 US-09-907-652-2	10 US-09-902-572A-2 Sequence 2,	10 US-09-902-979-2 Sequence 2,	10 US-09-905-123-2 Sequence 2,	10 US-09-905-449-2 Sequence 2,	10 US-09-903-806-2 Sequence 2,	10 US-09-904-992-2 Sequence 2,	10 US-09-906-777-2 Sequence 2,	10 US-09-903-603A-2 Seguence 2,	10 US-09-904-532-2 Sequence 2,	10 US-09-904-766-2 Sequence 2,	10 US-US-904-904-520A-2	10 US-09-903-562-2 Sequence 2,	10 US-09-906-618-2 Sequence 2,	10 US-09-907-728-2 Sequence 2,	10 US-09-904-805-2 Sequence 2,	10 US-US-904-938A-2 Sequence 2,	11 US-09-908-576-2 Sequence 2,	14 US-10-028-072-296 Seguence 29	14 US-10-140-808-296 Seguence 29	14 US-10-121-049-296 Sequence 29	14 US-10-123-904-296 Sequence 23	14 US-10-175-746-296 Sequence 25	14 US-10-176-918-296 Sequence 29	14 US-10-176-921-296 Sequence 29	14 US-IV-I3/-865-296 Sequence 25	14 US-10-142-431-296 Sequence 29	14 US-10-143-114-296 Sequence 29	14 US-10-142-419-296 Sequence 29	14 US-10-123-262-296 Sequence 23	14 US-10-121-050-296 Sequence 29	14 US-10-141-755-296 Sequence 29	14 US-10-143-032-296 Sequence 29	14 US-10-123-236-296 Sequence 23	14 US-10-123-261-296 Sequence 29	14 US-10-140-921-296 Sequence 29	14 US-10-140-928-296 Sequence 29	14 US-10-121-045-296 Sequence 29	14 US-10-123-903-296 Sequence 29	14 US-10-124-819-296 Sequence 29	14 US-10-124-822-296 Sequence 29	14 US-10-140-925-296 Sequence 29	14 US-10-160-498-296 Seguence 25	14 US-10-124-824-296 Sequence 23
10 US-09-907-925-2 Sequence 2, 10 US-09-902-692-2 Sequence 2, 10 US-09-903-520-2 Sequence 2, 10 US-09-905-056-2 Sequence 2, 10 US-09-905-056-2 Sequence 2, 10 US-09-905-055-3-2 Sequence 2, 10 US-09-904-553-2	4.4 353 10 US-09-905-381-2 Sequence 2, 4.4 353 10 US-09-904-485-2 Sequence 2, 4.4 353 10 US-09-904-485-2 Sequence 2, 4.4 353 10 US-09-904-485-2 Sequence 2,	4.4 353 10 US-09-908-088-2 Sequence 2, 4.4 353 10 US-09-907-575-2 Sequence 2,	4.4 353 10 US-09-905-075-2 Sequence 2,	4.4 353 10 US-09-902-634-2 Sequence 2,	4.4 353 10 US-09-907-979-2 Sequence 2,	4.4 353 10 US-09-902-615-2 Sequence 2, 4.4 353 10 US-09-903-925-2 Sequence 2,	4.4 353 10 US-09-906-760A-2 Sequence 2,	4.4 353 10 US-09-903-823-2 Sequence 2, 4.4 353 10 US-09-907-652-2 Sequence 2,	4.4 353 10 US-09-902-572A-2 Sequence 2,	4.4 353 10 US-09-902-979-2 Sequence 2,	4.4 353 10 US-09-906-815A-2 Sequence 2,	4.4 353 10 US-09-905-449-2 Sequence 2,	4.4 353 10 US-09-903-806-2 Sequence 2,	4.4 353 10 US-09-904-992-2 Sequence 2,	4.4 353 10 US-09-906-777-2 Sequence 2,	4.4 353 10 US-09-903-603A-2 Seguence 2,	4.4 353 10 US-09-904-532-2 Sequence 2,	4.4 353 10 US-09-904-766-2 Sequence 2,	4.4 353 IO US-US-9U4-9ZOA-Z 4.4 353 IO US-U9-9U4-8ZOA-Z	4.4 353 10 US-09-903-562-2 Sequence 2,	4.4 353 10 US-09-906-618-2 Sequence 2,	4.4 353 10 US-09-907-728-2 Sequence 2,	4.4 353 10 US-09-904-805-2 Sequence 2,	4.4 353 10 US-UY-YU4-Y38A-2 SEQUENCE Z,	4.4 353 11 US-09-908-576-2 Sequence 2,	4.4 353 14 US-10-028-072-296 Sequence 29	4.4 353 14 US-10-140-808-296 Sequence 29	4.4 353 14 US-10-121-049-296 Sequence 29	4.4 353 14 US-10-123-904-296 Sequence 23	4.4 353 14 US-10-175-746-296 Sequence 25	4.4 353 14 US-10-176-918-296 Sequence 29	4.4 353 14 US-10-176-921-296 Sequence 29	4.4 353 I4 US-I0-I3/-865-296 Sequence 29	4.4 353 14 US-10-142-431-296 Sequence 29	4.4 353 14 US-10-143-114-296 Sequence 29	4.4 353 14 US-10-142-419-296 Sequence 29	4.4 353 14 US-10-123-262-296 Sequence 23	4.4 353 14 US-10-121-050-296 Sequence 29	4.4 353 14 US-10-141-755-296 Sequence 29	4.4 353 14 US-10-143-032-296 Sequence 29	4.4 353 14 US-10-123-108-296 Sequence 29	4.4 353 14 US-10-123-261-296 Sequence 29	4.4 353 14 US-10-140-921-296 Sequence 29	4.4 353 14 US-10-140-928-296 Sequence 29	4.4 353 14 US-10-121-045-296 Sequence 29	4.4 353 14 US-10-123-903-296 Sequence 25	4,4 353 14 US-10-124-819-296 Sequence 29	4.4 353 14 US-10-124-822-296 Sequence 29	4.4 353 14 US-10-140-925-296 Sequence 29	4.4 353 14 US-10-160-498-296 Sequence 29	4.4 353 14 US-10-124-824-296 Sequence 25
4.4 353 10 US-09-907-925-2 Sequence 2, 4.4 353 10 US-09-902-692-2 Sequence 2, 4.4 353 10 US-09-903-65-20 Sequence 2, 4.4 353 10 US-09-905-056-2 Sequence 2, 4.4 353 10 US-09-905-056-2 Sequence 2, 4.4 353 10 US-09-904-553-2 Sequence 2, 4.4 353 10 US-09-904-553-2 Sequence 2, 4.4 353 10 US-09-904-553-2	7 54.4 353 10 US-09-90S-381-2 Sequence 2, 54.4 353 10 US-09-904-485-2	7 54.4 353 10 US-09-905-755-2 Sequence 2, 7 54.4 353 10 US-09-907-575-2 Sequence 2,	7 54.4 353 10 US-09-905-075-2 Sequence 2, 7 54.4 353 10 US-09-902-759-2 Sequence 2,	7 54.4 353 10 US-09-902-634-2 Sequence 2,	7 54.4 353 10 US-09-907-979-2 Sequence 2,	/ 54.4 353 10 US-09-902-615-2 Sequence 2, 7 54.4 353 10 US-09-903-925-2 Sequence 2,	7 54.4 353 10 US-09-906-760A-2 Sequence 2,	7 54.4 353 10 US-09-903-823-2 Sequence 2, 7 54.4 353 10 US-09-907-652-2 Sequence 2,	7 54.4 353 10 US-09-902-572A-2 Sequence 2,	7 54.4 353 10 US-09-902-979-2 Sequence 2,	7 54.4 353 10 US-09-905-125-2 Sequence 2,	7 54.4 353 10 US-09-905-449-2 Sequence 2,	7 54.4 353 10 US-09-903-806-2 Sequence 2,	7 54.4 353 10 US-09-904-9922-2 Sequence 2, 7 54.4 353 10 HS-09-904-838-2 Sequence 2,	7 54.4 353 10 US-09-906-777-2 Sequence 2,	7 54.4 353 10 US-09-903-603A-2 Sequence 2,	7 54.4 353 10 US-09-904-532-2 Sequence 2,	7 54.4 353 10 US-09-904-766-2 Sequence 2,	7 54 4 353 10 US-US-904-32UA-2 SEGUENCE 2,	7 54.4 353 10 US-09-903-562-2 Sequence 2,	7 54.4 353 10 US-09-906-618-2 Sequence 2,	7 54.4 353 10 US-09-907-728-2 Sequence 2,	7 54.4 353 IO US-09-904-805-2 Sequence 2,	7 54.4 353 10 US-US-VG-V38A-2	7 54.4 353 11 US-09-908-576-2 Sequence 2,	7 54.4 353 14 US-10-028-072-296 Sequence 29	7 54.4 353 14 US-10-140-808-296 Sequence 29	7 54.4 353 14 US-10-121-049-296 Sequence 29	7 34.4 333 14 03-10-123-904-236 Sequence 23	7 54.4 353 14 US-10-175-746-296 Sequence 25	7 54.4 353 14 US-10-176-918-296 Sequence 29	7 54.4 353 14 US-10-176-921-296 Sequence 29	/ 54.4 555 I4 US-IO-I3/-865-296 Sequence 25	7 54.4 353 14 US-10-142-431-296 Semience 29	7 54.4 353 14 US-10-143-114-296 Sequence 29	7 54.4 353 14 US-10-142-419-296 Sequence 29	/ 54.4 353 14 US-10-123-262-296 Sequence 23	7 54.4 353 14 US-10-121-050-296 Sequence 29	7 54.4 353 14 US-10-141-755-296 Sequence 29	7 54.4 353 14 US-10-143-032-296 Sequence 29	/ 54.4 353 14 US-10-123-236-296 Sequence 29	7 54.4 353 14 US-10-123-261-296 Sequence 29	7 54.4 353 14 US-10-140-921-296 Sequence 29	7 54.4 353 14 US-10-140-928-296 Sequence 29	7 54.4 353 I4 US-IO-IZI-045-296 Sequence 23	7 54.4 353 14 US-10-123-903-296 Sequence 25	7 54.4 353 14 US-10-124-819-296 Sequence 29	7 54.4 353 14 US-10-124-822-296 Sequence 29	7 54.4 353 14 US-10-140-925-296 Sequence 29	7 54.4 353 14 US-10-160-498-296 Seguence 25	/ 54.4 353 I4 US-IU-I24-824-296 Sequence 25

600	quence 296, quence 296,	quence 296, quence 296,	quence 296, quence 296,	quence 296, quence 296,	quence 296,	quence 296,	quence 296,	quence 296,	quence 296,	quence 296, quence 296,	quence 296,	quence 296,	quence 296, quence 296,	quence 296,	quence 296,	quence 296, quence 296,	quence 296,	quence 296,	quence 296,	quence 296,	quence 296,	quence 296,	quence 296,	quence 296, quence 296,	quence 296, quence 296,	quence 296,	quence 296,	equence 296, equence 296,	ence 296, ence 296,	equence 296,	equence 296, equence 296,	equence 296,	equence 296, equence 296,	equence 296,	equence 296,	equence 296,	equence 296,	equence 296, equence 296,	Tuence 2
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 Sequence 2, Application US/10126845

Sequence 2, Application US/10126845

Publication No. US20030181367A1

GENERAL INFORMATION;

APPLICANT: — TANGELIA, Imelda J.

APPLICANT: — FIDILIA, IMENBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

FILE REFERENCE: E1067/20058

CURRENT APPLICATION NUMBER: US/10/126,845

CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 119

SEQ ID NO 2

SEQ ID NO 2

LENGTH: 15

TYPE: PRT
 Sequence 3, Application US/10126845

Publication No. US20030181367A1

GENERAL INFORMATION:
APPLICANT: Clambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: HOUGHLEN, Richard
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: B1067/20058
CURRENT APPLICATION NUMBER: US/10/126,845
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin version 3.1
SEQ ID NO 3.
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 Length 15;
 Length 15
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 ; OTHER INFORMATION: membrane translocating peptide US-10-126-845-2
 Query Match 100.0%; Score 68; DB 14; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 15; Conservative 0; Mismatches 0;
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Pred. No. 0.00029;
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US-10-157-794-296
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OTHER INFORMATION: membrane transloci
FEATURE:
NAME/KEY: MOD_RES

LOCATION: (15)...(15)

OTHER INFORMATION: linked to FITC-LC
US-10-126-845-3
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 ORGANISM: Artificial Sequence
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Best Local Similarity
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 RESULT 2
US-10-126-845-3
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 LENGTH: 15
 FEATURE:
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 APPLICANT: CUMONE SAILY.
APPLICANT: CUMONE SAILY.
APPLICANT: CUMMONE SAILY.
APPLICANT: CUMMONE SAILY.
TITLE OF INVENTION: LIPLO-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
CURRENT APPLICATION NUMBER: US/10/136,187
CURRENT APPLICATION NUMBER: US 60/287,786
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 15
 APPLICANT: Harvie, Bierzol.

APPLICANT: Paul, Ralph
APPLICANT: O'Mahory, Daniel, J.

TITLE OF INVENTION: AND METHODE OR THEIR PRODUCTION
FILE REPERBUCE: 226272005300
CURRENT FILING DATE: 2002-09-13
FILE REPERBUCE: 2002-09-13
FILE REPERBUCE: 2002-09-13
FRIOR APPLICATION NUMBER: US 60/287,786
FRIOR PAPLICATION NUMBER: US 60/287,786
FRIOR PELING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARRE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 15
 Score 68; DB 15; Length 15;
Pred. No. 0.00029;
 Indels
 DOCATION: 1 COTHER INFORMATION: Lysine is attached to galactose US-10-136-187-6
 Query Match
100.0%; Score 68, DB 15;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0;
 ; OTHER INFORMATION: Synthetic Construct US-10-136-187-2
 OTHER INFORMATION: Synthetic Construct
 ; Sequence 2, Application US/10136187; Publication No. US20030203865A1; GENERAL INFORMATION:
 Sequence 6, Application US/10136187; Publication No. US20030203865A1; GENERAL INFORMATION:
 100.0%;
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
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 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
 Query Match
Best Local Similarity
 NAME/KEY: VARIANT
 TYPE: PRT
 TYPE: PRT
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 APPLICANT: O'Mahony, Daniel J.
APPLICANT: Tambfin, Imelda J.
APPLICANT: Tambfin, Imelda J.
APPLICANT: Fambfin, Imelda J.
APPLICANT: Fambfin, Imelda J.
APPLICANT: Fambfin, Richard.
APPLICANT: HOUGHEN, RICHARD.
FILE NEFERENCE: BIO67/20058
CURRENT APPLICATION NUMBER: US/10/126,845
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin version 3.1
SEQ ID NO 60
 GENERAL INFORMATION:

APPLICANT: O'MANDAY, Daniel J.

APPLICANT: Manday, Daniel J.

APPLICANT: Einhkin, Tmelda J.

APPLICANT: Einila, Clemencia

APPLICANT: Houghten, Richard

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

FILE REPERENCE: E1067/20058
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 100.0%; Score 68; DB 14; Length 15; 100.0%; Pred. No. 0.00029; tive 0; Mismatches 0; Indels
 100.0%; Score 68; DB 14; Length 15; 100.0%; Pred. No. 0.00029;
 0; Indels
 0; Indels
0; Mismatches
 0; Mismatches
 CURRENT APPLICATION NUMBER: US/10/126,845
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin version 3.1
SEQ ID NO 61
 LOCATION: (1).7(15)
COTHER INFORMATION: D form amino acid
US-10-126-845-60
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1 LOCATION: (1)...(15)
1 OTHER INFORMATION: D form amino acid
US-10-126-845-61
 Sequence 61, Application US/10126845; Publication No. US20030181367A1
 ; Sequence 60, Application US/10126845; Publication No. US20030181367A1
 OTHER INFORMATION: D form peptide
 FEATURE: OTHER INFORMATION: D form peptide
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
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 1 KKAAAVLLPVLLAAP 15
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 Query Match
Best Local Similarity 100.09
Matches 15; Conservative
15; Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
 NAME/KEY: MISC_FEATURE
 US-10-126-845-60
 US-10-126-845-61
Matches
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 Sequence 33, Application US/10136187

| Publication No. US20030203865A1
| Publication No. US20030203865A1
| GENERAL INPORMATION:
| APPLICANT: Harvie, Pierrot
| APPLICANT: Cudmore, Sally
| TILLE OF INVENTION: LIFID-COMPRESING DRUG DELIVERY COMPLEXES
| TILLE OF INVENTION: LIFID-COMPRESING PROPUCTION
| FILE REFERENCE: 2267206390
| CURRENT APPLICATION NUMBER: US/10/136,187
| CURRENT FILING DATE: 2002-09-13
| PRIOR PILING DATE: 2001-04-30
| NUMBER OF SEQ ID NOS: 45
| SEQ ID NO 33
| SEQ ID NO 33
| LENGTH: 15
 Sequence 34, Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:

APPLICANT: FBUI, Raiph
APPLICANT: TEUINCE PAID

APPLICANT: TEUINCE PAID

APPLICANT: TEUINCE PAID

APPLICANT: CUGMORE, SAILY

APPLICANT: CUMANON, Daniel J.

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

FILE REPERBNCE: 226272005300

CURRENT APPLICATION NUMBER: US/10/136,187

CURRENT FILING DATE: 2001-09-13

PRIOR APPLICATION NUMBER: US 60/287,786

PRIOR APPLICATION NUMBER: US 60/287,786

PRIOR APPLICATION NUMBER: US 60/287,786

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 34

LENGTH: 15
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 ; OTHER INFORMATION: Lysine is attached to Cholesteryl-succinyl
US-10-136-187-33
 Length 15;
 Indels
 Indela
Pred. No. 0.00029; Mismatches 0;
 100.0%; Score 68; DB 15; 100.0%; Pred. No. 0.00029;
 Mismatches
 OTHER INFORMATION: Synthetic Construct PEATURE:
 OTHER INFORMATION: Synthetic Construct
 ö
Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 Query Match
Best Local Similarity 100...
Best Local Similarity 100...
 NAME/KEY: VARIANT
 NAME/KEY: VARIANT
 US-10-136-187-34
 US-10-136-187-33
 PEATURE:
 RESULT 10
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 Gaps
 Gaps
 Sequence 13. Application US/10136187

Sequence 13. Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:

APPLICANT: BAT'G, Pierrot

APPLICANT: BAT'G, Pierrot

APPLICANT: GUGMOTE, Bally

APPLICANT: OLIMOTION: AND METHODS FOR THEIR PRODUCTION

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

FILE REPERBENCE: 226272063300

CURRENT APPLICATION NUMBER: US 60/287,786

FRIOR PILING DATE: 2001-09-13

PRIOR FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FaetSEQ for Mindows Version 4.0

SEQ ID NO 13

LENGTH: 15

CONTACT: CONTACTOR CONT
 ö
 RESULT 7

US-10-136-187-12

Sequence 12, Application US/10136187

Sequence 12, Application US/10136187

Sequence 12, Application US/20030203865A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Quantum Order of the content of the co
 ö
 Query Match
100.0%; Score 68; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0; Indels
 100.0%; Score 68; DB 15; Length 15;
 Indels
 FEATURE:
NAME/KEY: VARIANT
LOCATION: 1
OCHER INFORMATION: Lysine is attached to DOPE-succinyl
 ö
 Mismatches
 OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
 ö
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 15; Conservative
 RESULT 8
US-10-136-187-13
 US-10-136-187-12
 US-10-136-187-13
 TYPE: PRT
 Query Match
 Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 15
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 Query Match
Best Local Similarity 100.0
Matches 15; Conservative
 NAME/KEY: VARIANT
 LOCATION:
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 Gaps
 Gaps
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 Sequence 36, Application US/10136187
Sequence 36, Application US/10136187
Publication No. US20030203865A1
GENERAL INFORMATION:
APPLICANT: Harvie, Pierrock
APPLICANT: Daul, Ralph
APPLICANT: Co'Mahony, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
FITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
FILE REFERENCE: 22622005300
CURRENT APPLICATION NUMBER: US/10/136,187
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US 60/287,786
PRIOR PILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
 PEATURE:
NAMBE/KEY: VARIANT
LOCATION: 1
COTHER INFORMATION: Lysine is attached to Cholesteryl-succinyl
FEATURE:
 Query Match 100.0%; Score 68; DB 15; Length 15; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 15; Conservative 0; Mismatches 0; Indels
 APPLICANT: Harvie, Pierrot
APPLICANT: Baul, Ralph
APPLICANT: Cudmore, Sally
APPLICANT: Cudmore, Sally
APPLICANT: O'MANDON, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: LAPID-COMPRISING POR THEIR PRODUCTION
FILE REPERENCE: 226272005300
CURRENT APPLICATION NUMBER: US/10/136,187
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION DATE: 2001-04-30
 100.0%; Score 68; DB 15; Length 15; 100.0%; Pred. No. 0.00029; tive 0; Mismatches 0; Indels
; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to DOPE-succinyl
US-10-136-187-34.
 NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
 NAME/KET: VARIANT
LOCATION: (1)...(15)
COTHER INFORMATION: D amino acid sequence
VS-10-136-187-38
 OTHER INFORMATION: Synthetic Construct
 ; Sequence 35, Application US/10136187; Publication No. US20030203865A1; GENERAL INFORMATION:
 TYPE: PRT ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 Query Match
Best Local Similarity 100.0
Matches 15; Conservative
 US-10-136-187-35
 US-10-136-187-36
 SEQ ID NO 35
LENGTH: 15
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 Gaps
 Gaps
 Sequence 37, Application US/10136187

Sequence 37, Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:
APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: O'MANON, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: LIPID-COMPRISING PRODUCTION
FILE REFERENCE: 226272063300
CURRENT PILING DATE: 2002-09-13
CURRENT PILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 37
LENGTH: 15
 ö
 ö
) NAME/KEY: VARIANT

) LOCATION: 1

) CTHER INFORMATION: Lysine is attached to DSPE-PEGSK-succinyl

US-10-136-187-36
 Length 15;
 Length 15;
 ; OTHER INFORMATION: Lysine is attached to DMPB-PEG5K-succinyl
US-10-136-187-37
 US-10-136-187-38
US-10136-187-38
US-10-136-187-38
Sequence 38, Application US/10136187
Publication No. US20030203865A1
GENERAL INFORMATION:
APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Cudmore, Sally
APPLICANT: Cudmore, Sally
APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: Lirplo-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 226272005300
 0; Indels
 Query Match 100.0%; Score 68; DB 15; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 15; Conservative 0; Mismatches 0;
 100.0%; Score 68; DB 15;
100.0%; Pred. No. 0.00029;
tive 0; Mismatches 0;
FEATURE:
OTHER INFORMATION: Synthetic Construct
FEATURE:
 FEATURE: OTHER INFORMATION: Synthetic Construct
```

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TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE REPERRNCE: P26,479-B USA CURRENT APPLICATION NUMBER: US/10/764,235 CURRENT FILING DATE: 2004-01-23 PRIOR PILING DATE: 2004-01-27 PRIOR RILING DATE: 2000-09-27 PRIOR FILING DATE: 12000-09-27 PRIOR PILING DATE: 12009-09-27 NUMBER OF SEQ ID NOS: 59 SOFTWARE: PACENTIN NOS: 59 SOFTWARE: PACENTIN VERSION 3.1 SEQ ID NOS: 59
 Gaps
 Gaps
 Sequence 2. Application US/10850873

Sequence 2. Application US/10850873

Sublication No. US20050025821A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Sally

APPLICANT: O'BAND METHODS FOR THEIR PRODUCTION

ITILE OF INVENTION: LIPTO-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPTO-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

FILE REPREBREE: 226272005300

CURRENT PILING DATE: 2004-05-20

PRIOR PLING DATE: 2004-05-20

PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSEQ for Windows Version 4.0

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SOFTWARE: FastSEQ for Windows Version 4.0
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 Length 15;
 Length 15;
 Indels
 Indels
 Query Match 100.0%; Score 68; DB 17; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 15; Conservative 0; Mismatches 0;
 TYPE: PRT
MCANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: membrane translocating peptide
 100.0%; Score 68; DB 16;
100.0%; Pred. No. 0.00029;
ttive 0; Mismatches 0;
 OTHER INFORMATION: Synthetic Construct
 ; NAME/KEY: MOD RES
; LOCATION: (15)...(15)
; OTHER INFORMATION: linked to FITC-LC
US-10-764-235-2
 RESULT 18
US-10-850-873-6
Squence 6, Application US/10850873; Publication No. US20050025821A1
; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 Query Match
Best Local Similarity 100.0
Matches 15; Conservative
 US-10-850-873-2
 US-10-850-873-2
 LENGTH: 15
 LENGTH: 15
 FEATURE:
 RESULT 17
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 Gaps
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 APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Paul, Ralph
APPLICANT: Commore, Sally
APPLICANT: O'Mahory, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 226272005300
CURRENT APPLICATION NUMBER: US/10/136,187
CURRENT PILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US 60/207,786
PRIOR SEQ ID NOS: 45
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 15
 ; OTHER INFORMATION: Lygine is attached to DSPE-PEG5K-succinyl
US-10-136-187-38
 NAME/KEY: VARIANT
1 LOCATION: 1
1 OTHER INFORMATION: Lysine is attached to DMPE-PEG5K-succinyl
US-10-136-187-39
 Query Match
100.0%; Score 68; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0; Indels
 Length 15;
 Indels
 Query Match
100.0%; Score 68; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0;
 CURRENT APPLICATION NUMBER: US/10/136,187
CURRENT FILING DATE: 2002-09-13
PRIOR PILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 15
 OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
 US-10-136-187-39

Sequence 39, Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:
 US-10-764-235-2

Sequence 2, Application US/10764235

Publication No. US20040138132A1

GENERAL INFORMATION:

APPLICANT: O'Mahony, Daniel J.

APPLICANT: Lambkin, Imelda J.
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 NAME/KEY: VARIANT
 LOCATION: 1
 TYPE: PRT
 FEATURE:
 RESULT 16
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WS-10-850-873-13

| Sequence 13, Application US/10850873
| Sequence 13, Application US/10850873
| Sequence 13, Application US/10850873
| Sequence 13, Application No. US20050025821A1
| GENERAL INFORMATION:
| APPLICANT: Harvie, Pierrot
| APPLICANT: Cudmore, Sally
| APPLICANT: O'Mahony, Daniel J.
| TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
| TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
| TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
| TITLE OF INVENTION: LIPID-COMPRISING DRUG DATE: 2002-04-30
| CURRENT FILING DATE: 2002-04-30
| PRIOR APPLICATION NUMBER: US/10/136,187
| PRIOR APPLICATION NUMBER: US/10/136,187
| PRIOR PILING DATE: 2001-04-30
| NUMBER OF SEQ ID NOS: 45
| SEQ ID NO 13
| LENGTH: 15
 JOURGANT: HATVIE, PIETOL

APPLICANT: Harvie, Pietrot

APPLICANT: Paul, Ralph

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Daniel J.

TITLE OF INVENTION: LIPLD-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPLD-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

FILE REFERENCE: 226272005300

CURRENT APPLICATION NUMBER: US/10/850,873

CURRENT FILING DATE: 2004-05-20

PRIOR PELLING DATE: 2002-04-30

PRIOR PELLING DATE: 2002-04-30

PRIOR PELLING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 33

LENGTH: 15

***CRANTED TO THE NUMBER: US ADDITED TO THE NUMBER: PAGE TO THE NOS: 45

***CRANTED TO THE NUMBER: DATE: 2001-04-30

***CRANTED TO THE NUMBER: US ADDITED TO THE NUMBER: PAGE TO THE NOS: 45

***CRANTED TO THE NUMBER: PAGE TO THE NOS: 45

***CRANTED TO THE NUMBER: PAGE TO THE NOS: 45

***CRANTED TO THE NUMBER: PAGE TO THE NOS: 45

***CRANTED TO THE NUMBER: PAGE TO THE NOS: 45

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***CRANTED TO THE NUMBER: PAGE TO THE NOS: 45

***CRANTED TO THE NOS: 45

***CRANTED TO THE NOS: 45

***CRANTED TO THE NUMBER: PAGE TO THE NOS: 45

***CRANTED TO
 ; OTHER INFORMATION: Lysine is attached to Cholesteryl-succinyl US-10-850-873-33
 Length 15;
 Query Match 100.0%; Score 68; DB 17; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 15; Conservative 0; Mismatches 0;
) OTHER INFORMATION: Synthetic Construct US-10-850-873-13
 OTHER INFORMATION: Synthetic Construct
 Sequence 33, Application US/10850873
Publication No. US20050025821A1
GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 NAME/KEY: VARIANT
 TYPE: PRT
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 APPLICANT: Paul, Ralph
APPLICANT: Cudmore, Sally
APPLICANT: Cudmore, Sally
APPLICANT: Cudmore, Dally
TITLE OF INVENTION: LIFID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: LIFID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: LIFID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: LIFID-COMPRISING
TITLE OF INVENTION: LUMBER: US/10/850,873
CURRENT APPLICATION NUMBER: US/10/136,187
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2001-04-30
 ö
 Sequence 12, Application US/10850873

Publication No. US20050025821A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Candinore, Sally

APPLICANT: Condinore, Sally

APPLICANT: Condinore, Sally

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

CURRENT APPLICATION NUMBER: US/10/650,873

CURRENT FILING DATE: 2004-05-20

PRIOR FILING DATE: 2004-04-30

PRIOR FILING DATE: 2001-04-30
 Query Match 100.0%; Score 68; DB 17; Length 15; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 15; Conservative 0; Mismatches 0; Indels
 Length 15;
 0; Indels
 // LOCATION: 1
// OTHER INFORMATION: Lysine is attached to DOPE-succinyl
US-10-850-873-12
 NAME/KEY: VARIANT
1 LOCATION: 1
1 OTHER INFORMATION: Lysine is attached to galactose 08-10-850-873-6
 ch 10.0%; Score 68; DB 17; 1 Similarity 100.0%; Pred. No. 0.00029; 15; Conservative 0; Mismatches 0;
 NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 15
 NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 15
 OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
 ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
APPLICANT: Harvie, Pierrot
 Best Local Similarity
 NAME/KEY: VARIANT
 RESULT 19
US-10-850-873-12
 Query Match
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FEATURE:

Matches

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1 KKAAAVLLPVLLAAP 15

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Gaps
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 RESULT 24

US-10-850-873-36

US-10-850-873-36

Sequence 36, Application US/10850873

Publication No. US2005002821A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: O'Nahony, Daniel J.

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION UNMERR: US/10/136,187

PRIOR APPLICATION NUMBER: US 60/287,786

PRIOR APPLICATION NUMBER: US 60/287,786

PRIOR APPLICATION NUMBER: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSEQ for Windows Version 4.0
 ö
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 NAME/KEY: VARIANT
LOCATION: 1
OTHER INFORMATION: Lysine is attached to Cholesteryl-succinyl
) OTHER INFORMATION: Lysine is attached to DSPE-PEG5K-succinyl US-10-850-873-36
 Length 15;
 Length 15;
 Sequence 37, Application US/10850873
Publication No. US20050025821A1
GENERAL INFORMATION:
APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Cudmore, Sally
APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
 Indela
 Query Match 100.0%; Score 68; DB 17; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 15; Conservative 0; Mismatches 0;
 Query Match
100.0%; Score 68; DB 17;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0;
 ; NAME/KEY: VARIANT; LOCATION: (1)...(15); LOCATION: (1)...(15); OTHER INFORMATION: D amino acid sequence US-10-850-873-35
 FEATURE: OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVILPVILAAP 15
 NAME/KEY: VARIANT
 US-10-850-873-37
 FEATURE:
 RESULT 25
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 Gaps
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 Sequence 35, Application US/10850873

Sequence 35, Application US/10850873

Publication No. US20050025821A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DRUG DRUG DRUG DRUG DATE: 2004-05-20

CURRENT APPLICATION NUMBER: US/10/136,187

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2001-04-30

PRIOR FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE FRAESQ for Windows Version 4.0
 APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Paul, Ralph
APPLICANT: Condinore, Sally
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 26272005300
CURRENT APPLICATION NUMBER: US/10/85.87
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 34
LENGTH: 15
Query Match
100.0%; Score 68; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0; Indels
 Query Match
100.0%; Score 68; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0; Indels
 ; OTHER INFORMATION: Lysine is attached to DOPE-succinyl US-10-850-873-34
 OTHER INFORMATION: Synthetic Construct
 Sequence 34, Application US/10850873
Publication No. US20050025821A1
GENERAL INFORMATION:
 ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 NAME/KEY: VARIANT LOCATION: 1
 US-10-850-873-34
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 Sequence 38, Application US/10850873
| Sequence 38, Application US/10850873
| Publication No. US20050025821A1
| GENERAL INFORMATION:
| APPLICANT: Harvie, Pierrot
| APPLICANT: Cudmore, Sally
| APPLICANT: Cudmore, Sally
| APPLICANT: Cudmore, Daniel J.
| TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
| TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
| FILE REPERBNCE: 22627208300
| CURRENT APPLICATION NUMBER: US/10/850,873
| CURRENT APPLICATION NUMBER: US/10/136,187
| PRIOR PILING DATE: 2002-04-30
| PRIOR PILING DATE: 2002-04-30
| NUMBER OF SEQ ID NOS: 45
| SOFTWARE FREECO for Windows Version 4.0
| SEQ ID NO 38
 ; OTHER INFORMATION: Lysine is attached to DMPE-PEG5K-succinyl
US-10-850-873-37
 ; NAME/KEY: VARIANT
; LOCATION:
; JOCATION: Lysine is attached to DSPE-PEG5K-succinyl
US-10-850-873-38
 Length 15;
 Length 15;
 Indels
 Indels
AND METHODS FOR THEIR PRODUCTION
 100.0%; Score 68; DB 17; 100.0%; Pred. No. 0.00029;
 100.0%; Score 68; DB 17;
100.0%; Pred. No. 0.00029;
 Mismatches
 FILE REPERENCE: 226272005300
CURRENT APPLICATION NUMBER: US/10/850,873
CURRENT FILING DATE: 2004-05-20
PRIOR APPLICATION NUMBER: US/10/136,187
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2002-04-30
PRIOR PILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 15
 Mismatches
 OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
PEATURE:
 TYPE: PRT ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
 NAME/KEY: VARIANT LOCATION: 1
 US-10-850-873-38
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RESULT 27

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APPLICANT: O'Mahony, Daniel J.
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Pinilla, Clemencia
APPLICANT: Pinilla, Clemencia
TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: AGENTS
CURRENT APPLICATION NUMBER: US/10/955,656
CURRENT APPLICATION NUMBER: US/10/955,656
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 APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Paul, Ralph
APPLICANT: Cudmore, Sally
APPLICANT: Cudmore, Sally
APPLICANT: Cudmore, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS, FOR THEIR PRODUCTION
FILE REFRENCE: 22627205500
CURRENT APPLICATION NUMBER: US/10/850,873
CURRENT FILING DATE: 2004-05-20
PRIOR PILING DATE: 2002-04-30
PRIOR PILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
 ; OTHER INFORMATION: Lysine is attached to DMPE-PEGSK-succinyl
US-10-850-873-39
 Length 15;
 Length 15;
 Indela
 Indels
 Score 68; DB 17;
Pred. No. 0.00029;
 100.0%; Score 68; DB 17;
100.0%; Pred. No. 0.00029;
tive 0; Mismatches 0;
 ; FEATÜRE:
; OTHER INFORMATION: membrane translocating peptide
US-10-955-656-2
 Mismatches
 OTHER INFORMATION: Synthetic Construct
 PRIOR APPLICATION NUMBER: 10/126, 845
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-27
PRIOR PILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin version 3.1
Sequence 39, Application US/10850873 Publication No. US20050025821A1 GENERAL INFORMATION:
 Sequence 2, Application US/10955656 Publication No. US20050101762A1 GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 Query Match
Best Local Similarity 100.
Matches 15; Conservative
 NAME/KEY: VARIANT
 SEQ ID NO 39
LENGTH: 15
 LOCATION:
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Sequence 6.1 Application US/10955656

Bublication No. US20050101762A1

GENERAL INPORMATION:

APPLICANT: Cambrin, Imelda J.

APPLICANT: Lambkin, Imelda J.

APPLICANT: Houghten, Richard

TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY

TITLE OF INVENTION: AGENTS

FILE REFERENCE: P26,481-A USA

CURRENT FILING DATE: 2004-09-30

PRIOR FILING DATE: 2000-04-19

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 119

SOFTWARE PATENTIN VERSION 3.119
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 RESULT 32
US-10-126-645-48
ISAQUENCE 48, Application US/10126845
SEQUENCE 48, Application No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: O'MAHONY, Daniel J.
APPLICANT: Pinilla, Clemencia
APPLICANT: Houghten, Richard
TITLE OF INVENTION: REMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20058
 Gaps
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 Length 15;
 Length 15;
 Indels
 Indels
 Query Match
100.0%; Score 68; DB 17;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0;
 100.0%; Score 68; DB 17;
100.0%; Pred. No. 0.00029;
vative 0; Mismatches 0;
 FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (1). [15)

OTHER INFORMATION: D form amino acid
US-10-955-656-60
 NAME/KEY: MISC_FEATURE
; LOCATION: (1)...(15)
; OTHER INFORMATION: D form amino acid
US-10-955-656-61
 OTHER INFORMATION: D form peptide
 OTHER INFORMATION: D form peptide
ORGANISM: Artificial Sequence FEATURE:
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 1 KKAAAVLLPVLLAAP 15
 Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
 RESULT 31
US-10-955-656-61
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 US-10-930-050-00

Sequence 60. Application US/10955656

Publication No. US2005101762A1

GENERAL INFORMATION:
APPLICANT: O'MAHOON, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Houghten, Richard
TITLE OF INVENTION: CONUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
TITLE OF INVENTION: AGENTS
FILER REFERENCE: P26, 481-A USA
CURRENT FILING DATE: 2004-09-30
PRIOR PAPLICATION NUMBER: 10/126, 845
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 09/671, 089
PRIOR PILING DATE: 1009-09-27

PRIOR PILING DATE: 1099-09-27

NUMBER OF SEQ ID NOS: 119
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
LENGTH: 15
 Sequence 3, Application US/10955656

Publication No. US200S0101762A1

GENERAL INFORMATION:

APPLICANT: O'Mahony, Daniel J.

APPLICANT: D'Mahony, Daniel J.

TITLE OF INVENTION: AGENTS

FILE REFERENCE: P26,481-A USA

CURRENT FILING DATE: 2004-09-30

PRIOR FILING DATE: 2002-04-19

PRIOR PILICATION NUMBER: 09/671,089

PRIOR FILING DATE: 1999-09-27

PRIOR PILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 119

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LUMBER OF DATE: DATE

LUMBER DATE

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 Gaps
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 Length 15;
 Indels
 Score 68; DB 17;
Pred. No. 0.00029;
 OTHER INFORMATION: membrane translocating peptide
 0: Mismatches
 ; NAME/KEY: MOD RES
; LOCATION: (15)...(15)
; OTHER INFORMATION: linked to FITC-LC
US-10-955-656-3
 Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
 ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
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Gaps

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APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Paul, Ralph
APPLICANT: Commore, Sally
APPLICANT: O'Mahory, Daniel J.
APPLICANT: O'Mahory, Daniel J.
APPLICANT: O'Mahory, Daniel J.
APPLICANT: O'Mahory, Daniel J.
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 226272005300
CURRENT APPLICATION NUMBER: US/10/136,187
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US 60/287,786
 Length 16;
 Length 16;
 IndelB
 Indels
 ; OTHER INFORMATION: Lysine is attached to galactose US-10-136-187-7
 Score 68; DB 15;
Pred. No. 0.00031;
 100.0%; Score 68; DB 15;
100.0%; Pred. No. 0.00031;
tive 0; Mismatches 0;
 ; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to dansyl
US-10-136-187-28
 Mismatches
 PRIOR APPLICATION NUMBER: US 60/287,786
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PastSEQ for Windows Version 4.0
EEQ ID NO 7
LENGTH: 16
 OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
 Sequence 28, Application US/10136187
Publication No. US20030203865A1
GENERAL INFORMATION:
 Sequence 32, Application US/10136187
Publication No. US20030203865A1
GENERAL INFORMATION:
 ö
 2002-09-13
 Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
 TYPE: PRT ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 2 KKAAAVLLPVLLAAP 16
 1 KKAAAVLLPVLLAAP 15
 Query Match
Best Local Similarity 100.0
Matches 15; Conservative
 APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Cudmore, Sally
 CURRENT FILING DATE:
 NAME/KEY: VARIANT LOCATION: 1
 NAME/KEY: VARIANT
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 Gaps
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 RESULT 33
US-10-136-187-3

Sequence 3, Application US/10136187

Sequence 3, Application US/20030203865A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: O'Mahony, Daniel J.

TITLE OF INVENTION: LIPLO-COMPRISING DRUG DELIVERY COMPLEXES

FILE REFERENCE: 226272005300

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: US 60/287,786

PRIOR RILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SOPTWARE: FABREEQ for Windows Version 4.0

1 DATE OF THE MAN OF THE OF
 FEATURE: OTHER INFORMATION: dansylated membrane translocating peptide
 Score 68; DB 14; Length 16; Pred. No. 0.00031;
 100.0%; Score 68; DB 15; Length 16; 100.0%; Pred. No. 0.00031; tive 0; Mismatches 0; Indels
 Sequence 7, Application US/10136187
Publication No. US20030203865A1
GENERAL INFORMATION:
APPLICANT: Harvie, Pierrot
APPLICANT: Cudmore, Sally
APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: LIPID-COMPRISING PRODUCTION
FILE REFERENCE: 226722063300
CURRENT APPLICATION NUMBER: US/10/136,187
 Indela
 Mismatches
CURRENT APPLICATION NUMBER: US/10/126,845
UNUMBER OF SEQ ID NOS: 119
SOFTWARE: PATENT NOS: 119
) OTHER INFORMATION: Synthetic Construct US-10-136-187-3
 Query Match
Best Local Similarity 100.0%; Part Local Similarity 100.0%; Partches 15; Conservative 0;
 TYPE: PRT
ORGANISM: Artificial Sequence
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: dansylated
US-10-126-845-48
 TYPE: PRT
ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 2 KKAAAVLLPVLLAAP 16
 1 KKAAAVLLPVLLAAP 15
 2 KKAAAVLLPVLLAAP 16
 Conservative
 Query Match
Best Local Similarity
Matches 15; Conserv
 US-10-136-187-7
 FEATURE:
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Gaps

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Sequence 48, Application US/10764235

Sequence 48, Application US/10764235

Sequence 48, Application US/20040138132A1

GENERAL INFORMATION:
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imedad J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: P26,479-B USA
CURRENT APPLICATION NUMBER: US/10/764,235

CURRENT FILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: 09/671,089

PRIOR PILING DATE: 1999-09-27

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PatentIn version 3.1

SEQ ID NO 48

LENGTH: 16
APPLICANT: Lambkin, Imelda J.

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: P26.479-B USA
CURRENT APPLICATION NUMBER: US/10/764,235
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: 09/671,089
PRIOR APPLICATION NUMBER: 60/156,246
PRIOR APPLICATION NUMBER: 60/156,246
PRIOR PILING DATE: 1999-09-27
ROWBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
 Gaps
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 FEATURE: OTHER INFORMATION: dansylated membrane translocating peptide
 Length 16;
 Length 16;
 Indels
 0; Indels
 Query Match 100.0%; Score 68; DB 16; Best Local Similarity 100.0%; Pred. No. 0.00031; Matches 15; Conservative 0; Mismatches 0;
 100.0%; Score 68; DB 16; 100.0%; Pred. No. 0.00031;
 ; OTHER INFORMATION: membrane translocating peptide US-10-764-235-3
 Mismatches
 Sequence 3, Application US/10850873; Publication No. US20050025821A1; GENERAL INPORMATION:
APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
 ö
 i LOCATION: (1) \(\tilde{\capacita}\); (1)
i OTHER INFORMATION: dansylated
US-10-764-235-48
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 2 KKAAAVLLPVLLAAP 16
 2 KKAAAVLLPVLLAAP 16
 1 KKAAAVLLPVLLAAP 15
 Query Match
Best Local Similarity 100.0
"...he
 NAME/KEY: MOD_RES
 US-10-850-873-3
 FEATURE:
 RESULT 40
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 Sequence 91, Application US/10116275

Publication No. US20030211476A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Elan Pharmaceutical Technology
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Higgins, Liss
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and
TITLE OF INVENTION: Longostions Targeting Peyer's Patches and Methods and
CURRENT APPLICANT: 2002-10-04

NUMBER OF SEQ ID NOS: 349

SOFTWARE: PatentIn version 3.1

SEQ ID NO 91

LENGTH: 16
 TYPE: PRT ORGANISM: Artificial Sequence CRANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance Up OTHER INFORMATION: take Across the GIT" US-10-116-275-91
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 APPLICANT: O'Mahony, Daniel J.

TITLE OF INVENTION: LIFID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REPERRICE: 22672005300
CURRENT FILING DATE: 2002-09-13
CURRENT FILING DATE: 2002-09-13
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 16
 100.0%; Score 68; DB 15; Length 16; 100.0%; Pred. No. 0.00031;
 100.0%; Score 68; DB 15; Length 16; 100.0%; Pred. No. 0.00031; tive 0; Mismatches 0; Indels
 Indels
 COCATION: 1; LOCATION: 1; OTHER INFORMATION: Serine is attached to galactose US-10-136-187-32
 0; Mismatches
 FEATURE:
OTHER INFORMATION: Synthetic Construct
 Sequence 3, Application US/10764235; Publication No. US20040138132A1 GENERAL INFORMATION: APPLICANT: O'Mahony, Daniel J.
 ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 2 KKAAAVLLPVLLAAP 16
 1 KKAAAVLLPVLLAAP 15
 Query Match
Best Local Similarity 100.0°
Matches 15; Conservative
 Query Match
Best Local Similarity 100.
Matches 15; Conservative
 NAME/KEY: VARIANT
 US-10-116-275-91
 RESULT 38
US-10-764-235-3
 PRT
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NAME/KEY: VARIANT
 NAME/KEY: VARIANT
 TYPE: PRT
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 Gaps
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 Sequence 7, 3-7, 5 publication US/10850873
Fublication No. US20050025821A1
GENERAL INFORMATION:
APPLICANT: Paul, Ralph
APPLICANT: Cudmore, Sally
APPLICANT: Cudmore, Sally
APPLICANT: Cudmore, Sally
TITLE OF INVENTION: LIPTD-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: LiptD-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: Lab METHODS FOR THEIR PRODUCTION
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
CURRENT APPLICATION NUMBER: US/10/136,187
FRIOR FILING DATE: 2002-04-30
FRIOR FILING DATE: 2002-04-30
FRIOR FILING DATE: 2002-04-30
FRIOR FILING DATE: 2002-04-30
FRIOR FILING DATE: 2003-04-30
 ö
APPLICANT: O'MANON, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLES OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 22672063300
CURRENT APPLICATION NUMBER: US/10/850,873
CURRENT FILING DATE: 2004-05-20
PRIOR PRIOR PRICATION NUMBER: US/10/136,187
PRIOR APPLICATION NUMBER: US/0/10/136,187
PRIOR APPLICATION NUMBER: US 60/287,786
PRIOR PRILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 16
 100.0%; Score 68; DB 17; Length 16; 100.0%; Pred. No. 0.00031; tive 0; Mismatches 0; Indels
 Query Match 100.0%; Score 68; DB 17; Length 16; Best Local Similarity 100.0%; Pred. No. 0.00031; Matches 15; Conservative 0; Mismatches 0; Indels
 NAME/KEY: VARIANT

CCATION: 1

COTHER INFORMATION: Lysine is attached to galactose
(MS-10-850-873-7)
) OTHER INFORMATION: Synthetic Construct US-10-850-873-3
 OTHER INFORMATION: Synthetic Construct
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLAAP 15
 KKAAAVLLPVLLAAP 16
 1 KKAAAVLLPVLLAAP 15
 Best Local Similarity 100. Matches 15; Conservative
 Query Match
 FEATURE:
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RESULT 42 US-10-850-873-28

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Gaps
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 GENERAL INFORMATION.

JEDILOGANT: Harvie, Pierrot

APPLICANT: Harvie, Pierrot

APPLICANT: Harvie, Pierrot

APPLICANT: Gudmore, Sally

APPLICANT: Cudmore, Sally

APPLICANT: O'Mahony, Daniel J.

TITLE OF INVENTION: LIPLO-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPLO-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPLO-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPLO-COMPLEXES

TITLE OF ANDERICATION NUMBER: US,10,850,873

CURRENT FILING DATE: 2004-05-20

PRIOR APPLICATION NUMBER: US,10/136,187

PRIOR APPLICATION NUMBER: US,00/204,786

PRIOR APPLICATION NUMBER: US,00/204,30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 16
 APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Paul, Ralph
APPLICANT: Cudnore, Sally
APPLICANT: Cudnore, Sally
APPLICANT: Cudnore, Sally
APPLICANT: Cudnore, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 226272005300
CURRENT APPLICATION NUMBER: US/10/850,873
CURRENT PILING DATE: 2004-05-20
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 32
LENGTH: 16
 Length 16;
 Score 68; DB 17; Length 16; Pred. No. 0.00031;
 Indela
 ; LOCATION: 1
; OTHER INFORMATION: Serine is attached to galactose
US-10-850-873-32
 Query Match 100.0%; Score 68; DB 17; Best Local Similarity 100.0%; Pred. No. 0.00031; Matches 15; Conservative 0; Mismatches 0;
 ; OTHER INFORMATION: Lygine is attached to dansyl
US-10-850-873-28
 OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
 US-10-850-873-32
; Sequence 32, Application US/10850873
; Publication No. US20050025821A1
; GENERAL INFORMATION:
 100.0%;
 TYPE: PRT ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
US20050025821A
 1 KKAAAVLLPVLLAAP 15
 2 KKAAAVLLPVLLAAP 16
 Query Match
Best Local Similarity
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 Sequence 4, Application US/10126845
Publication No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Pinilla, Clemencia
APPLICANT: Pinilla, Richard
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REPRENCE: E1067/220058
CURRENT APPLICATION NUMBER: US/10/126,845
CURRENT FILING DATE: 2002-10-15
 Gaps
 Gaps
 US-10-850-873-30

US-10-850-873-30

Sequence 30, Application US/10850873

Publication No. US2005002821A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: O'MAHORY, Daniel J.

TITLE OF INVENTION: LIPD-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

FILE REFERENCE: 2267-206300

CURRENT APPLICATION NUMBER: US/10/136,187

PRIOR FILING DATE: 2004-05-20

PRIOR FILING DATE: 2004-03-00

PRIOR PILING DATE: 2001-04-30

PRIOR PILING DATE: 2001-04-30

PRIOR SEQ ID NOS: 45

SOFTWARE: FastSEQ for Windows Version 4.0
 ö
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 Length 17;
 Length 17;
 Indels
 Indels
 Query Match 100.0%; Score 68; DB 17;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 15; Conservative 0; Mismatches 0;
 Query Match
100.0%; Score 68; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 15; Conservative 0; Mismatches 0;
 i LOCATION: 1
; OTHER INFORMATION: Lygine is attached to dansyl
US-10-136-187-30
 NAME/KEY: VARIANT
LOCATION: 1
COATION: 1
USER INFORMATION: Lysine is attached to dansyl
US-10-850-873-30
OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
 TYPE: PRT
ORGANISM: Artificial Sequence
 NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
 1 KKAAAVLLPVLLAAP 15
 3 KKAAAVLLPVLLAAP 17
 1 KKAAAVLLPVLLAAP 15
 3 KKAAAVLLPVLLAAP 17
 NAME/KEY: VARIANT
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 Sequence 48 Application US/10955656

| Publication No. US20050101762A1
| GENERAL INFORMATION:
| APPLICANT: Lambkin, Imelda J. |
| APPLICANT: Lambkin, Imelda J. |
| APPLICANT: Lambkin, Imelda J. |
| APPLICANT: Houghten, Richard |
| TITLE OF INVENTION: CONUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY |
| TITLE OF INVENTION: CONUGATES OF MEMBRANE TRANSLOCATING AGENTS APPLICANT |
| TITLE OF INVENTION: CONUGATES OF MEMBRANE TRANSLOCATING AGENTS |
| FILE REPRENCE: PES, 481- AUSA |
| CURRENT APPLICATION NUMBER: US/10/955,656 |
| CURRENT PILING DATE: 2002-04-19 |
| PRIOR PELLING DATE: 2000-09-27 |
| PRIOR PELLING DATE: 2000-09-27 |
| PRIOR FILING DATE: 1999-09-27 |
| REAL OF SEQ ID NOS: 119 |
| SEQ ID NO 48 |
| LENGTH: 16 |
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 APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Paul, Ralph
APPLICANT: Commone, Sally
APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 256272005300
CURRENT APPLICATION NUMBER: US/10/136,187
FILE REPERSIONE: 2001-09-13
PRIOR PILING DATE: 2001-09-13
PRIOR PILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PASTSEQ for Windows Version 4.0
IBNGTH: 17
TYPE: PRT
CRANISM: Artificial Sequence
FEATURE:
 OTHER INFORMATION: dansylated membrane translocating peptide
 Query Match
100.0%; Score 68; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 15; Conservative 0; Mismatches 0; Indels
 Indels
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 Mismatches
 Sequence 30, Application US/10136187
Publication No. US20030203865A1
GENERAL INFORMATION:
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 FEATURE:
NOAME/KEY: MOD_RES
NOCATION: (1)...(1)
OTHER INFORMATION: dansylated
 ORGANISM: Artificial Sequence
 2 KKAAAVLLPVLLAAP 16
 1 KKAAAVLLPVLLAAP 15
 2 KKAAAVLLPVLLAAP 16
 1 KKAAAVLLPVLLAAP 15
 15; Conservative
 US-10-955-656-48
 US-10-136-187-30
 TYPE: PRT
 Matches
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 Sequence 62, Application US/10126845
Publication No. US20030181367A1
Publication No. US20030181367A1
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imedad J.
APPLICANT: Houghten, Richard
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REPERENCE: E1067/20058
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin version 3.1
 Sequence 108, Application US/10126845
Publication No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Pinilla, Clemencia
APPLICANT: Houghten, Richard
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20058
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: D-form peptide; Comprises opioid peptide
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CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 108
LENGTH: 19
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US-10-126-845-62
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TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 15; Conservative
 RESULT 49
US-10-126-845-108
 US-10-126-845-62
 SEQ ID NO 62
LENGTH: 19
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Sequence 92, Application US/10116275
; Sequence 92, Application US/10116275
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; GENERAL INFORMATION:
; APPLICANT: Branchutical Technology
; APPLICANT: Brayden, David
; APPLICANT: Brayden, David
; APPLICANT: Brayden, David
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and Mchlods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and Mchlods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; CURRENT APPLICATION WORBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
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; SEQ ID NO SE ALENCE PATCH VERSION 3.1
; LENGTH: 19
) OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance.Up
) OTHER INFORMATION: take Across the GIT"
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Pred. No. 0.00037;
 Mismatches
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Job time : 89.6562 secs
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OTHER INFORMATION: D-form amino acid
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Matches 15; Conservative C
 ORGANISM: Artificial Sequence
 NAME/KEY: MOD_RES
LOCATION: (19)...(19)
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US-10-126-845-108
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 GenCore version 5.1.6
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Sequence 24, Application US/08928958

Sequence 24, Application US/08928958

Sequence 24, Application US/08928958

Sequence 24, Application US/08928958

Setent No. 5877282

SERENAL INFORMATION:
APPLICANT: BLAKE, JAMES

APPLICANT: BLAKE, JAMES

TITLE OF INVENTION: PERTIND INHIBITORS OF NUCLEAR PROTEIN

TITLE OF INVENTION: PEANLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSE: 90 MIDDLEFIELD ROAD, SUITE 200

STREET: 90 MIDDLEFIELD ROAD, SUITE 200

CITY, MELLO PARK
; Sequence 24, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION;
APPLICANT: O'Mahony, Daniel J.
APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REPERENCE: E1067/20018
; CURRENT PELICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 12000-09-27
; PRIOR PILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 24
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 Gaps
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 Query Match
100.0%; Score 76; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels
 STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 12-SEP-1997
CLASSIFICATION SATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L:
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
 , OTHER INFORMATION: membrane translocating peptide US-09-671-089-24
 TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
 TYPE: PRT
ORGANISM: Artificial Sequence
 US-08-928-958-24
 FEATURE:
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PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
METHODS OF USE THEREOF
 Sequence 1, Application US/09072429

Patent No. 5962415

GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
 Gaps
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 Length 30;
 Indela
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
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COMPOTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION NUMBER: US 60/026978
FILING DATE: CO-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELECOMMUNICATION NUMBER: 5998-0019
 COUNTRY: USA
ZIP: 08543-4000
COMPUTER READABLE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,429
 DB 2;
 TITLE OF INVENTION: PEPTIDE INHIBITORS OF TITLE OF INVENTION: TRANSLACATION HAVING TITLE OF INVENTION: METHODS OF USE THEREC NUMBER OF SEQUENCES: 24
CARRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ROBING & ASSOCIATES STREET: 90 MIDDLEPIELD ROAD, SUITE 200
 1 KKKRKAAAAVLLP-VLLA 17
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 TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7812
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Matches 14; Conservative
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 STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
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 MENLO PARK
 linear
 amino acid
 USA
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 STATE: C. COUNTRY:
 US-09-072-429-1
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 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION:
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
TITLE OF INVENTION: INMUNOSUPPRESSANT AND METHODS OF USE THEREOF
INVERS OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: ADDRESSE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
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STREET: P.O. Box 4000
CITY: Princeton
STRIE: New Jersey
COUNTRY: TS. PROPPY disk
COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
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CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/09/072,429
FILING DATE: OH-MAY-1998
CLASSIFICATION NUMBER: 34.363
FELENCHNEY/AGRAT INFORMATION:
NAME: Klein, Christopher A.
REFERENCE/DOCKET NUMBER: 34.363
FELECOMMUNICATION NUMBER: 34.363
FELECOMMUNICATION NUMBER: ON0141b
TELECOMMUNICATION INFORMATION:
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 ;
 Score 53.5; DB 2; Length 29;
Pred. No. 0.055;
0; Mismatches 3; Indels
 Query Match 70.4%; Score 53.5; DB 2; Length 29; Best Local Similarity 77.8%; Pred. No. 0.055; Matches 14; Conservative 0; Mismatches 3; Indels
 NADLER, STEVEN G.
CLEAVELAND, JEFFREY S.
BLAKE, JAMES
 Sequence 24, Application US/09072429 Patent No. 5962415
 Sequence 1, Application US/08928958
Patent No. 5877282
GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
 2 KKKRKVAAVALLPAVLLA 19
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 1 KKKRKAAAAVLLP-VLLA 17
 TELEFAX: (609) 252-4526
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LENGTH: 29 amino acids
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Best Local Similarity 77.8%;
Matches 14; Conservative
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; MOLECULE TYPE: peptide
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 US-09-072-429-24
 APPLICANT:
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 US-09-072-429-24
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US-08-928-958-1
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OTHER INFORMATION: linked to FITC-LC
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 Sequence 3, Application US/09671089

Sequence 3, Application US/09671089

Patent No. 6780846

GENERAL INFORMATION:
APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20018

CURRENT FILING DATE: 2000-09-27

PRIOR PAPLICATION NUMBER: 06/156,246

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 59

SOUTHARE: Patentin version 3.1

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GENERAL INFORMATION:
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APPLICANT: Dambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: CANDON MADER: US/09/671,089
CURRENT FILING DATE: 2000-09-27
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PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
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 70.4%; Score 53.5; DB 2; Length 30; 77.8%; Pred. No. 0.057; tive 0; Mismatches 3; Indels
 Query Match 69.7%; Score 53; DB 4; Length 16; Best Local Similarity 85.7%; Pred. No. 0.036; Matches 12; Conservative 1; Mismatches 1; Indels
 OTHER INFORMATION: membrane translocating peptide
 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KLein. Christopher A.
REGISTRATION NUMBER: 34,363
REFERENCE/DOCKET NUMBER: ON0141b
TELECOMUNICATION INFORMATION:
TELEPHONE: (609) 252-3714
TELEPAX: (609) 252-37
 2 KKKRKVAAVALLPAVLLA 19
 1 KKKRKAAAAVLLP-VLLA 17
 ORGANISM: Artificial Sequence
 4 RKAAAAVLLPVLLA 17
 Best Local Similarity 77.8
Matches 14; Conservative
 US-09-671-089-48
 US-09-671-089-3
 US-09-072-429-1
 -09-671-089-3
 Query Match
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 Sequence 4, Application US/09671089

Patent No. 6780846

Patent No. 6780846

Patent No. 6780846

APPLICANT: O'MATON: Daniel J.

APPLICANT: Lambkin, Imelda J.

APPLICANT: O'MATON: WEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM FILE REPERENCE: E1067/20018

CURRENT APPLICATION NUMBER: US/09/671,089

CURRENT FILING DATE: 1999-09-77

PRIOR PULICATION NUMBER: 60/156,246

PRIOR FILING DATE: 1999-09-77

NUMBER OF SEC ID NOS: 59
 % Sequence 2, Application US/09671089

patent No. 67804871081

patent No. 67804871081

patent No. Mahony, Daniel J.

APPLICANT: Lambkin, Imalda J.

TILLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

FILE REPERENCE: E1067/20018

CURRENT APPLICATION NUMBER: US/09/671,089

CURRENT PILING DATE: 2000-09-27

PRIOR PILING DATE: 1999-09-27
 Gaps
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FEATURE:
OTHER INFORMATION: dansylated membrane translocating peptide
 67.1%; Score 51; DB 4; Length 15; 92.3%; Pred. No. 0.071;
 Score 53; DB 4; Length 16; Pred. No. 0.036;
 1; Indels
 OTHER INFORMATION: membrane translocating peptide
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Gaps

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RESULT 13
US-08-928-956-2

J Sequence 2, Application US/08928958

J Sequence 2, Application US/08928958

J EALENT NO. 5877282

J GENERAL INFORMATION:

APPLICANT: HAFER, STEVEN G.

APPLICANT: HAFER, OWAR K.

TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROBINS & ASSOCIATES

STEEFT: 90 MIDDLEFIELD ROAD, SUITE 200
 RESULT 12
US-09-671-089-5
i Sequence 5, Application US/09671089
i Patent No. 6780846
i GENERAL INFORMATION:
APPLICANT: O'MAHONY, Daniel J.
APPLICANT: O'MAHONY, Daniel J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFRENCE: E1067/20018
CURRENT APPLICATION NUMBER: US/09/671,089
CURRENT FILING DATE: 2000-09-27
PRIOR PILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
SEQ ID NO S. 54
 Length 16;
 FEATURE:
; OTHER INFORMATION: membrane translocating peptide, cyclic US-09-671-089-5
 2; Indels
 2; Indels
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
**APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
 Score 47; DB 4;
Pred. No. 0.32;
 Pred. No. 0.28;
 0; Mismatches
 0; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INPORMATION:
 ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EIBM PC compatible
 Best Local Similarity 84.6%;
Matches 11; Conservative
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
 5 KAAAAVLLPVLLA 17
 1 KKCAAVLLPVLLA 13
 5 KAAAAVLLPVLLA 17
 1 KKCAAVLLPVLLA 13
 MENLO PARK
 USA
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 COUNTRY:
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 Sequence 7, Application US/09671089

Patent No. 6780846

GENERAL INFORMATION

APPLICANT: O'Mahony, Daniel J.

APPLICANT: Lambkin, Imalda J.

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

FILE REFERENCE: E1067/20018

CURRENT APPLICATION NUMBER: US/09/671,089

CURRENT FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/156,246

PRIOR APPLICATION NUMBER: 60/156,246

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin version 3.1

LENGTH: 14
 Sequence 58, Application US/09671089
Facent No. 6780846
GENERAL INFORMATION:
APPLICANT: O'MAHONY, Daniel J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REPERENCE: ELOG/120108
CURRENT APPLICATION NUMBER: US/09/671,089
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/156,246
PRIOR PILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
SEQ ID NO 58
LENGTH: 14
TYPE: PRI
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 FEATURE:
; OTHER INFORMATION: membrane translocating peptide, cyclic internal
US-09-671-089-58
 , OTHER INFORMATION: membrane translocating peptide, cyclic internal
US-09-671-089-7
 ö
 Query Match 61.8%; Score 47; DB 4; Length 14; Best Local Similarity 84.6%; Pred. No. 0.28; Matches 11; Conservative 0; Mismatches 2; Indels
 4; Length 19;
 61.8%; Score 47; DB 4; Length 14;
 1; Indels
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: membrane translocating peptide
US-09-671-089-4
 Score 51; DB 4
Pred. No. 0.09;
 0; Mismatches
 ORGANISM: Artificial Sequence
 Query Match 67.1%;
Best Local Similarity 92.3%;
Matches 12; Conservative
 ORGANISM: Artificial Sequence
 S KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 5 KAAAAVLLPVLLA 17
 1 KKCAAVLLPVLLA 13
 RESULT 11
US-09-671-089-58
 RESULT 10
US-09-671-089-7
SEQ ID NO 4
 Query Match
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ORGANISM: Artificial Sequence
 Query Match 57.9%;
Best Local Similarity 78.6%;
Matches 11; Conservative
 TYPE: PRT
ORGANISM: Artificial Sequence
 4 RKAAAAVLLPVLLA 17
 RGIPAAVLLPVLLA 17
 RESULT 16
US-10-116-288A-20
 SEQ ID NO 20
 rype: prt
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 Sequence 2, Application US/09072429

Patent No. 5962415

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
INFIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN TITLE OF INVENTION:
INMINISTRACE OF INVENTION:
INMINISTRACE OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
 Gaps
 ;
 ö
 Length 26;
 Length 26;
 4; Indels
 4; Indels
 COUNTRY: USA

ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,429
FILING DATE: 04-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Klein, Christopher A.
REFERENCE/DOCKET NUMBER: 040141b
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 252-4526
INFORMATION FOR SEQ ID NO: 2:
 61.8%; Score 47; DB 2;
70.6%; Pred. No. 0.53;
iive 1; Mismatches
 Query Match 61.8%; Score 47; DB 2; Best Local Similarity 70.6%; Pred. No. 0.53; Matches 12; Conservative 1; Mismatches
 ADDRESSEE: Bristol-Myers Squibb Company
NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEPHONE: (650) 325-7823
TELEPAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 2:
ELENGTH: 26 amino acids
TYPE: amino acids
 ||| ||| |:| ||||
1 KKKYKAAVALLPAVLLA 17
 1 KKKRKAAAAVLLPVLLA 17
 1 KKKYKAAVALLPAVLLA 17
 1 KKKRKAAAAVLLPVLLA 17
 SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
 Query Match
Best Local Similarity 70.6
Matches 12; Conservative
 STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
 single
 MOLECULE TYPE: peptide
 TYPE: amino acid
 linear
 STRANDEDNESS:
 USA
 COUNTRY:
 US-09-072-429-2
 JS-09-072-429-2
 RESULT 14
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Sequence 4, Application US/10116288A Patent No. 6780843
 TYPÉ: PRT
ORGANISM: Artificial Sequence
 JOURNAL: Nature Biotechnology
 Query Match
Best Local Similarity 100.03
The Conservative
 LOCATION: (1)..(10) PUBLICATION:
 8 AAVLLPVLLA 17
 ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
 Patent No. 6432680
 RESULT 19
US-10-116-288A-4
 US-09-562-868-4
 ENGTH: 10
 SEQ ID NO 4
 FEATURE:
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 Sequence 4, Application US/09186170

Sequence 4, Application US/09186170

Patent No. 624858

GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Rojas, Mauricio
APPLICANT: Propertion
FILE APPLICANT: Proteins with Cell Membrane Translocating of
FILE REFERENCE: VU9841
CURRENT APPLICATION NUMBER: US/09/186,170
CURRENT APPLICATION NUMBER: 00/080,083
EARLIER PILLNG DATE: 1998-11-04
SEALLIER PILLNG DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGRIF 100

LENGRIF 100
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 APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
 ORGANISM: Artificial Sequence FEATURE: OFFICE OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of peptide which transports proteins OTHER INFORMATION: through the cell membrane into the cell.
; OTHER INFORMATION: sequence of peptide which transports proteins ; OTHER INFORMATION: through the cell membrane into the cell. US-10-116-288A-20
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 FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(10)
PUBLICATION: (1)..(10)
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
 Query Match 57.9%; Score 44; DB 4; Length 25; Best Local Similarity 76.9%; Pred. No. 1.5; Matches 10; Conservative 1; Mismatches 2; Indels
 56.6%; Score 43; DB 3; Length 10; 100.0%; Pred. No. 0.87; tive 0; Mismatches 0; Indels
 Sequence 4, Application US/09562868
Patent No. 6432680
GENERAL INFORMATION:
 JOURNAL: Nature Biotechnology VOLUME: 16
 S KAAAAVLLPVLLA 17
 4 RGIAAVLLPVLLA 16
 RELEVANT RESIDUES: 1 TO 12
 Best Local Similarity 100.
Matches 10; Conservative
 1 AAVLLPVLLA 10
 8 AAVLLPVLLA 17
 ISSUE: April PAGES: 370-375 DATE: 1998-04-01
 US-09-186-170-4
 US-09-562-868-4
 TYPE: PRT
 Query Match
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GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Lin, Yao-Zhong
APPLICANT: Bolashue, John P.
APPLICANT: Rojas Mauticio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
TITLE OF INVENTION: Procteins with Cell Membrane Translocating Activity"
TILLE REFERENCE: 22000.0097U3
CURRENT APPLICATION NUMBER: 09/562,868
PRIOR APPLICATION NUMBER: 09/562,868
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
 ö
TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
FILE REFERENCE: 22000.0097U2
CURRENT APPLICATION NUMBER: US/09/562,868
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/080,083
PRIOR APPLICATION NUMBER: 60/080,083
PRIOR APPLICATION NUMBER: 09/186,170
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 10
 Gaps
 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence of peptide which transports proteins
OTHER INFORMATION: through the cell membrane into the cell.
 ö
 TYPE: PRT
VEGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Ami
OTHER INFORMATION: sequence of peptide which transports pro
OTHER INFORMATION: through the cell membrane into the cell.
NAME/KEY: PEPTIDE
LOCATION: (1)..(10)
 AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
 Length 10;
 0; Indels
 56.6%; Score 43; DB 4; 100.0%; Pred. No. 0.87;
 100.0%; Pred. No. v.v.
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US-10-116-288A-5
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 Gaps
 OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of peptide which transports proteins OTHER INFORMATION: through the cell membrane into the cell.
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 LOCATION: (1)...(10)
PUBLICATION: (1)...(10)
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
 FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(11)
PUBLICATION INCOMATION:
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
 56.6%; Score 43; DB 4; Length 10; 100.0%; Pred. No. 0.87; tive 0; Mismatches 0; Indels
 Length 11;
 0; Indels
 56.6%; Score 43; DB 3;
100.0%; Pred. No. 0.96;
tive 0; Mismatches
 ORGANISM: Artificial Sequence FEATURE:
 JOURNAL: Nature Biotechnology VOLUME: 16
 Query Match
Best Local Similarity 100.0
Matches 10; Conservative
 RELEVANT RESIDUES: 1 TO 12
 Query Match 56.6
Best Local Similarity 100.
Matches 10; Conservative
 1 AAVLLPVLLA 10
 8 AAVLLPVLLA 17
 1 AAVLLPVLLA 10
 8 AAVLLPVLLA 17
 i ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-10-116-288A-4
NAME/KEY: PEPTIDE
 ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
 US-09-186-170-5
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RESULT 21

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Sequence, Application US/0552868

Sequence, Application US/0552868

Perent No. 643260.

Sequence Application US/0552868

Perent No. 643260.

Perent No. 643220.

Peren
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TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
FILE REPERBURG: VU0841
CURRENT APPLICATION NUMBER: US/09/186,170
CURRENT PILING DATE: 1998-11-04
EARLIER APPLICATION NUMBER: 60/080,083
EARLIER FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 18
 OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of peptide which transports proteins OTHER INFORMATION: through the cell membrane into the cell. NAME/KEY: PEPTIDE LOCATION: (1)...(12) PUBLICATION INFORMATION: AUTHORS: Rojas, M. et al.
 LOCATION: (1)...(12)
PUBLICATION INFORMATION:
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Am OTHER INFORMATION: sequence of peptide which transports prOTHER INFORMATION: through the cell membrane into the cell
 Length 12;
 0; Indels
 DB 3;
 56.6%; Scor.
100.0%; Pred. No. 1,
... 0; Mismatches
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE:
 RELEVANT RESIDUES: 1 TO 12
 Query Match
Best Local Similarity 100.
 8 AAVLLPVLLA 17
 1 AAVLLPVLLA 10
 NAME/KEY: PEPTIDE
 ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
 RESULT 25
US-09-562-868-1
 SEQ ID NO 1
LENGTH: 12
 US-09-186-170-1
 FEATURE:
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 Sequence 15, Application US/09671089

Parent No. 6780846

GENERAL INFORMATION:
APPLICANT: O'MAHONY, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICATION: WINBER: US/09/671,089

CURRENT FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 59

SOFTWARE PALENT VERSION 3.1
 Gaps
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 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence of peptide which transports proteins
OTHER INFORMATION: through the cell membrane into the cell.
FEATURE:
NAME/KEY: PEPTIDE
 GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
 ö
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 LOCATION: (1)...(11)
BUBLICATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Enginearing of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
 56.6%; Score 43; DB 4; Length 11; 100.0%; Pred. No. 0.96;
 DB 4; Length 11; 0.96;
 Indels
 ; OTHER INFORMATION: membrane translocating peptide US-09-671-089-15
 56.6%; Score 43; DB 100.0%; Pred. No. 0.9 iive 0; Mismatches
 0; Mismatches
 Sequence 1, Application US/09186170 Patent No. 624858
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.
Matches 10; Conservative
 Query Match
Best Local Similarity 100.
Matches 10; Conservative
 1 AAVLLPVLLA 10
 8 AAVLLPVLLA 17
 8 AAVLLPVLLA 17
 ; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-10-116-288A-5.
 US-09-671-089-15
 RESULT 24
US-09-186-170-1
 SEQ ID NO 15
LENGTH: 11
SEQ ID NO 5
LENGTH: 11
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Gaps

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sequence 1, Application US/10116288A

Sequence 1, Application US/10116288A

GENERAL INFORMATION:

APPLICANT: Lin, Yao-Zhong

APPLICANT: Lin, Yao-Zhong

APPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

TITLE OF INVENTION WINBER: US/10/116,288A

CURRENT FILING DATE: 12098-10-04

PRIOR FILING DATE: 12098-11-04

PRIOR FILING DATE: 1998-03-31

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.0

LENTH: 12
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 Sequence 1, Application US/09671089
; Sequence 1, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
 APPLICANT: O'MAHORY, Daniel J.
 APPLICANT: Lambkin, Imelda J.
 TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REPERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT PILING DATE: 2000-09-27
; PRIOR PPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
 Gaps
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 FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1). (12)
PUBLICATION: (1). (12)
AUTHORS: Rojas, M. et al.
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Am:
OTHER INFORMATION: sequence of peptide which transports pro
OTHER INFORMATION: through the cell membrane into the cell
 56.6%; Score 43; DB 4; Length 12; 100.0%; Pred. No. 1; 0; Indels tive 0; Mismatches 0; Indels
 TYPE: PRT
ORGANISM: Artificial Sequence
 Best Local Similarity 100.
Matches 10; Conservative
 8 AAVLLPVLLA 17
 , DATE: 1998-04-01
US-10-116-288A-1
 RESULT 28
US-10-116-288A-1
 US-09-671-089-1
 Query Match
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 S-09-997-465B-4
Sequence 4, Application US/09997465B
Sequence 4, Application US/09997465B
Sequence 4, Application US/09997465B
Sequence 5.673574cF
Sequence 4, Application Secondary Secondary Sequence 4, Applicant Secondary Sec
 WS-10-083-889-8
Sequence 8, Application US/10083889
Sequence 8, Application US/10083889
Patchet No. 6673894
Fatch No. 6673894
GENERAL INFORMATION:
TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
TITLE OF INVENTION: UNMBER: US/10/083,889
CURRENT APPLICATION NUMBER: US 60/271,798
FRIOR APPLICATION NUMBER: US 60/271,798
FRIOR PILING DATE: 2001-02-27
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 8
SEQ ID NO 8
LENGTHAR: 12
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 Query Match 56.6%; Score 43; DB 4; Length 12; Best Local Similarity 100.0%; Pred. No. 1; Matches 10; Conservative 0; Mismatches 0; Indels
TITLE: "Genetic Engineering of Proteins with Cell Membrane
 56.6%; Score 43; DB 4; Length 12; 100.0%; Pred. No. 1; 0; Mismatches 0; Indels tive
 Score 43; DB 4; Length 12;
Pred. No. 1;
0; Mismatches 0; Indels
 0; Indels
 56.6%; Score 43; 100.0%; Pred. No.
 TITLE: Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
 Query Match
Best Local Similarity 100.
Matches 10; Conservative
 Query Match
Best Local Similarity 100.
Matches 10; Conservative
 1 AAVLLPVLLA 10
 8 AAVLLPVLLA 17
 1 AAVLLPVLLA 10
 8 AAVLLPVLLA 17
 8 AAVLLPVLLA 17
 ORGANISM: Homo sapiens
 ; ORGANISM: Mammalian
US-10-083-889-8
 ; ISSUE: April
; PAGES: 370-375
; DATE: 1998-04-01
US-09-562-868-1
 US-09-997-465B-4
 SEQ ID NO 4
 TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 1; Matches 10; Conservative 0; Mismatches
 RESULT 32
US-09-671-089-59
 FEATURE:
 RESULT 34
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 RESULT 30
US-09-611-089-14

i Sequence 14, Application US/09671089

j Patent No. 6780846

i GENERAL INFORMATION:
APPLICANT: O'MAHONY, Daniel J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20018

CURRENT APPLICATION NUMBER: US/09/671,089

CURRENT APLICATION NUMBER: 06/156,246

PRIOR PILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin Version 3.1

EENGTH: 12
 Sequence 16, Application US/09671089
; Sequence 16, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION
; APPLICANT: O'MADONY, Daniel J.
; APPLICANT: C'MADONY, Daniel J.
; TITLE OF INFORMING, IMENBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; TILE OF INFORMING, INFORMARE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 12
 Gaps
 Gaps
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 Length 12;
 56.6%; Score 43; DB 4; Length 12; 100.0%; Pred. No. 1; 0; Indels cive 0; Mismatches 0; Indels
 0; Indels
 ; OTHER INFORMATION: membrane translocating peptide US-09-671-089-1
 FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-09-671-089-14
 ; FEATURE:
; OTHER INFORMATION: membrane translocating peptide
US-09-671-089-16
 4;
 DB
1,
 0; Mismatches
 Score 43;
Pred. No.
 Query Match 56.6%; 8
Best Local Similarity 100.0%;
Matches 10; Conservative 0
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 ORGANISM: Artificial Sequence
 TYPE: PRT ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.
Matches 10; Conservative
 1 AAVLLPVLLA 10
 8 AAVLLPVLLA 17
 ||||||||||
1 AAVLLPVLLA 10
 8 AAVLLPVLLA 17
 US-09-671-089-16
SEQ ID NO 1
LENGTH: 12
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 ઠે
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 Sequence 59, Application US/09671089
; Sequence 59, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'MANONY, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REPREMENTS: 81067/2010 B
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 2000-09-27
; PRIOR PILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOGTWARE: Patentin version 3.1
; SEQ ID NO 59
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 Gaps
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 Gaps
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 RESULT 33
US-10-144-549-19
i Sequence 19, Application US/10144549
i Patent No. 6835810
i GENERAL INFORMATION:
APPLICANT: GeneShuttle Biopharm, Inc.
ITILE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
FILE REFERENCE: MBHB 02-340
CURRENT APPLICATION NUMBER: US/10/144,549
CURRENT FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 12
 DB 4; Length 12;
1;
0; Indels
 Length 12;
 Indels
 0; Indels
 ; OTHER INFORMATION: membrane translocating peptide US-09-671-089-59
 TYPE: PRT ORGANISM: Kaposi's sarcoma-associated herpesvirus
 56.6%; Score 43; DB 4;
100.0%; Pred. No. 1;
tive 0; Mismatches
 ; NAME/KEY: MISC PEATURE
; OTHER INFORMATION: Kaposi FGF signal sequence
US-10-144-549-19
 56.6%; Score 43; DB 100.0%; Pred. No. 1; ative 0; Mismatches
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 Ouery Match
Best Local Similarity 100.
Matches 10; Conservative
 Query Match
Best Local Similarity 100.
Matches 10; Conservative
 3 AAVLLPVLLA 12
 17
 8 AAVLLPVLLA 17
 3 AAVLLPVLLA 12
 8 AAVLLPVLLA 17
```

US-09-671-089-6

56.6%; Score 43; DB 4; Length 12;

Query Match

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Gaps
 Gaps
 Sequence 7, Application US/09689730

Patent No. 6825024

GENERAL INFORMATION:

APPLICANT: SELIX, Motcharu

APPLICANT: SHINGAWA, Akira

TITLE OP INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR

FILE REFERENCE: 55-290P

CURRENT APPLICATION NUMBER: US/09/689,730

CURRENT PILING DATE: 2000-10-13

PRIOR APPLICATION NUMBER: US/08/448,489
 APPLICANT: SEIKI, Motoharu
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAWA, Akira
ITILE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
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 Ouery Match 56.6%; Score 43; DB 4; Length 456; Best Local Similarity 52.9%; Pred. No. 41; Matches 9; Conservative 4; Mismatches 4; Indels
 Score 41; DB 4; Length 30;
Pred. No. 5.4;
 Length 30;
 0; Indels
 2; Mismatches
PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 20502 LENGTH: 456
 ; Sequence 7, Application US/08448489; Patent No. 6184022; GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20502
 1 KKKRKAAAAVLLPVLLA 17
 :::|: | || ||||||
16 RERRERAGAVACPVLLA 32
 53.9%;
 53.9%;
 NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 30
 Query Match
Best Local Similarity 81.8
 :||||:||||
6 SAAAVVLPVLL 16
 6 AAAAVLLPVLL 16
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-689-730-7
 ; ORGANISM: Homo sapiens
US-08-448-489-7
 Query Match
Best Local Similarity
 US-09-689-730-7
 US-08-448-489-7
 SEQ ID NO 7
 셤
 셤
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 8
 Sequence 20502, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J.
APPLICANT: Marc J.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.131 65.0522,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
 ö
 ö
 Sequence 23, Application US/09671089
Patent No. 6780846
BATEN TO GOVERNION:
APPLICANT: O'MAHORY, Daniel J.
APPLICANT: Lambkin, Imelda J.
CURRENT PILING DATE: 10509/671,089
CURRENT FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
 APPLICANT: O'Nahony, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20018
CURRENT APPLICATION NUMBER: US/09/671,089
CURRENT FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
 Gaps
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 ;
0
 56.6%; Score 43; DB 4; Length 17; 100.0%; Pred. No. 1.5;
 DB 4; Length 13;
 ; OTHER INFORMATION: membrane translocating peptide, cyclic US-09-671-089-6
 0; Indels
 0; Indels
 FEATURE: OTHER INFORMATION: membrane translocating peptide
 Query Match 56.6%; Score 43; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches
 0; Mismatches
 Sequence 6, Application US/09671089
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 Best Local Similarity 100.
Matches 10; Conservative
 8 AAVLLPVLLA 17
 AAVLLPVLLA 10
 8 AAVLLPVLLA 17
 2 AAVLLPVLLA 11
 Patent No. 6780846
GENERAL INFORMATION:
 US-09-252-991A-20502
 US-09-671-089-23
 US-09-671-089-23
 SEQ ID NO 23
 SEQ ID NO 6
 Query Match
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Gaps
 RESULT 41
US-09-521-220-1
i Sequence 1, Application US/09521220
i Sequence 1, Application US/09521220
i Patent No. 6139348
i GENERAL INFORMATION:
i APPLICANT: WILL, Horst
i HINZMANN, Bernd
i TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
 ö
 Length 579;
 Score 41; DB 3; Length 5/5.
Pred. No. 1.1e+02;
 COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30
 NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/704,711
FILING DATE: CUNKNOWN-
APPLICATION NUMBER: DE 443898.1
FILING DATE: 21-0CT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NUMBER: GRANDOS, PARTICLE D.
 REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220
FILING DATE: 08-Mar-2000
CLASSIFICATION: <Unknown>
 NAME: GRANADOS, PALTICIA D.
REGISTRATION INUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202)672-5399
TELEPHONE: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acids
 21-OCT-1994
 17-MAR-1994
 TELECOMMUNICATION INFORMATION
 TELEPHONE: (202)672-5300
 TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acid
STRANDEDNESS: single
 TELEFAX: (202)672-5399
 Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
 ATTORNEY/AGENT INFORMATION
 :[|||:|||||
535 SAAAVVLPVLL 545
 6 AAAAVLLPVLL 16
 TOPOLOGY: linear
 US-08-704-711A-1
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 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLERIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLERIC ACID AND THERAPEUTICS
TITLE OF INVENTION: APPLICATION NUMBER: US,09/252,991A
CURRENT APPLICATION NUMBER: US,60/074,788
PRIOR APPLICATION NUMBER: US,60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19092
LENGTH: 421
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 Gaps
 Sequence 1, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION
APPLICANT: WILL, Horst
TITLE OF INVENTION: DAS EQUENCES: 22
CONRESPONDENCE ADDRESS:
ADDRESSEB: FOLOY & Lardner
STREET: 3000 K Street, N.W., Suite 500
STREET: 3000 K Street, N.W., Suite 500
STREET: B.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER: EADABLE FORM:
WEDIUM TYPE: IPOPY disk
COMPUTER: 1BMP PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PREPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 10-MAR.1995
PRICH APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 10-MAR.1995
PRICH APPLICATION DATA:
APPLICATION NUMBER: DE 44138838.1
FILING DATE: 11-MAR.1994
PRICH APPLICATION DATA:
APPLICATION DATA:
PRICH APPLICATION DATA:
FILING DATE: 11-MAR.1994
PRICH APPLICATION DATA:
FILING DATE: 11-MAR.1994
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 Query Match 53.9%; Score 41; DB 4; Length 421; Best Local Similarity 50.0%; Pred. No. 78; Matches 8; Conservative 4; Mismatches 4; Indele
 Indels
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 Mismatches
 4; Mismatches
 Sequence 19092, Application US/09252991A
Patent No. 6551795
 ..
 ; TYPE: PRT
; OKGANISM: Pseudomonas aeruginosa
US-09-252-991A-19092
 2 KKRKAAAAVLLPVLLA 17
 | ::|:|| | | :||
48 RRRRAAGAALRPAVLA 63
 9; Conservative
 6 AAAAVLLPVLL 16
 RESULT 39
US-09-252-991A-19092
 US-08-704-711A-1
Matches
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Sequence 1, Application US/08448489
Patent No. 618402
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SATO, Hiroshi
CURRENT SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT PILIOR DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
 Sequence 9, Application US/09211704A
Patent No. 6271014
GENERAL INFORMATION:
APPLICANT: Gesiar. Vis, Blandine Marie
APPLICANT: Caux, Christophe
APPLICANT: Caux, Christophe
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 10
 Score 41; DB 3; Length 582; Pred. No. 1.1e+02; Mismatches 0; Indels
 AUGRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
CITY: Palo Alto
STATE: California
COMPRES: BAJO4-104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.30
SOFTWARE: BA TOTO DATA:
APPLICATION NUMBER: US/09/211,704A
FILING DATE:
CLASSIFICATION: 435
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/211,704A
FILING DATE: 09-AN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0781K
TELECOMMULCATION INFORMATION:
METERPHONE: G600852-9196
TELERPHONE: G600852-9196
 LENGTH: 582 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
 53.9%;
 TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Query Match
Best Local Similarity #1.8
Matches 9; Conservative
 538 SAAAVVLPVLL 548
 6 AAAAVLLPVLL 16
 TYPE: PRT
ORGANISM: Homo sapiens
 RESULT 44
US-09-211-704A-9
 SEQ ID NO 1
LENGIH: 582
 US-08-448-489-1
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 Gaps
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 GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: WILL, HORE
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: DNA SEQUENCES 72
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLGY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Wachington
STATE: D.C.
COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BACCOMPALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BACCOMPALE FORM:
MEDIUM TYPE: Parentin Release #1.0, Version #1.30
COMPUTER: D.C.
COMPUTER: DATE: 20-NOV-1996
CURRENT APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: DE 443838.1
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: DE 4409663.1
PRIOR APPLICATION NUMBER: DE 4409663.1
PRIOR APPLICATION NUMBER: DE 4409663.1
PRIOR APPLICATION NUMBER: 20-OCT-1994
ATTORNEY/AGENT INPORMATION:
NAME: GRANADOS, Particia B)
REGISTRATION NUMBER: 26083/124
TELECOMMUTICATION NUMBER: 26083/124
TELECOMMUTICATION NUMBER: 26083/124
TELECOMMUTICATION NUMBER: 26083/124
TELECOMMUTICATION NUMBER: 26083/124
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 Query Match 53.9%; Score 41; DB 3; Length 579; Best Local Similarity 81.8%; Pred. No. 1.1e+02; Matches 9; Conservative 2; Mismatches 0; Indels
 Length 582;
 Query Match 53.9%; Score 41; DB 3; Length 582
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 0; Indels
TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-521-220-1
 %5-08-704-711A-2; Sequence 2, Application US/08704711A; Patent No. 6114159; GENERAL INFORMATION:
 TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 LENGTH: 582 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 TELEPHONE: (202)672-5399
 :||||:|||||
538 SAAAVVLPVLL 548
 :||||:|||||
535 SAAAVVLPVLL 545
 6 AAAAVLLPVLL 16
 6 AAAAVLLPVLL 16
 US-08-704-711A-2
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Gaps

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GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAMA, Akira
APPLICANT: SHINAGAMA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
 Sequence 84, Application US/09919497
Patent No. 6713883
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER FILE REFRENCE: B0801/725
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
 Score 41; DB 4; Length 582;
Pred. No. 1.1e+02;
2; Mismatches 0; Indels
 Length 582;
 53.9%; Score 41; DB 3; Length 582
81.8%; Pred. No. 1.1e+02;
".*.marches 0; Indels
 APPLICANT: Palotto. Michael T.
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
ITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
ITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND MET
ITLE OF INVENTION: OF USING SAME;
ITLE OF INVENTION: OF USING SAME;
ITLE REFERENCE: 6073.US.Pl.
CURRENT FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/814,394
PRIOR RILING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2: SE
 2; Mismatches
 ; Sequence 28, Application US/09391104; Patent No. 6399371; GENERAL INFORMATION:
 Sequence 1, Application US/09689730 Patent No. 6825024
 53.9%;
 Query Match
Best Local Similarity 81.8
Matches 9; Conservative
 :[|||:|||||
538 SAAAVVLPVLL 548
 Query Match 53.5
Best Local Similarity 81.6
Matches 9; Conservative
 :||||:|||||
538 SAAVVLPVLL 548
 6 AAAAVLLPVLL 16
 6 AAAAVLLPVLL 16
 TYPE: PRT

ORGANISM: Homo sapiens
US-09-391-104-28
 ORGANISM: Homo sapiens
 SEQ ID NO 84
LENGTH: 582
 RESULT 47
US-09-919-497-84
 US-09-919-497-84
 RESULT 48
US-09-689-730-1
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 Gaps
 Sequence 2, Application US/09521220
Patent No. 6399348
GENERAL INFORMATION:
APPLICANT: WILL, Horst
HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
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 STAIL.

COUNTRY: USA

ZUD1: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/521,220

FILING DATE: 08-Mar-2000

CLASSIFICATION: <UNnown>

Z1-OCT-1994

17-MAR-1994
 Score 41; DB 3; Length 582;
Pred. No. 1.1e+02;
2; Mismatches 0; Indels
 Query Match 53.9%; Score 41; DB 3; Length 582; Best Local Similarity 81.8%; Pred. No. 1.1e+02; Matches 9; Conservative 2; Mismatches 0; Indels
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
 ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGIGTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,711
FILING DATE: «Unknown»
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
 STRANDENESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-521-220-2
 LENGTH: 582 amino acids
 Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
 TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
 NUMBER OF SEQUENCES:
 :||||:|||||
538 SAAAVVLPVLL 548
 :||||:|||||
538 SAAAVVLPVLL 548
 6 AAAAVLLPVLL 16
; MOLECULE TYPE: peptide US-09-211-704A-9
 6 AAAAVLLPVLL 16
 US-09-521-220-2
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Gaps

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Search completed: June Job time : 36.875 secs
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 Sequence 20037, Application US/09252991A

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20037
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 US-09-270-767-41668
Sequence 41668, Application US/09270767
Sequence 41668, Application US/09270767
Sequence 41668, Application US/09270767
Sequence 41668, Application US/09270767
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: FILE Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270, 767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTHARE: PatentIN Ver. 2.0
SEQ ID NO 41668
 Gaps
 Gaps
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0
 13;
 Query Match 53.3%; Score 40.5; DB 4; Length 716; Best Local Similarity 42.9%; Pred. No. 1.6e+02; Matches 12; Conservative 2; Mismatches 1; Indels 13
 52.6%; Score 40; DB 4; Length 238;
 Length 582;
 0; Indels
 Score 41; DB 4; I
Pred. No. 1.1e+02;
2; Mismatches 0;
 ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-41668
 231 KKKKAAKILGPILALVALKAAALLPLL 258
 2 KKRKAA-----AAVLLPVLL 16
CURRENT APPLICATION NUMBER: US/09/689,730
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US/08/448,489
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 582
 TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
 TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
 Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
 :||||:|||||
538 SAAAVVLPVLL 548
 6 AAAAVLLPVLL 16
 ; ORGANISM: Homo sapiens
US-09-689-730-1
 RESULT 50
US-09-252-991A-20037
 US-09-252-991A-20037
 Query Match
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16 US-10-764-235-58 Sequence 17 US-10-955-656-7 Sequence 17 US-10-955-656-65 Sequence 14 US-10-126-845-5 Sequence	14 US-10-126-845-63 Sequence	15 US-10-116-275-93 Sequence	17 US-10-955-656-5 Sequence	17 US-10-955-656-63 Sequence	16 US-10-784-309A-1 Sequence	16 US-10-784-309A-2 Sequence	12 US-10-136-18/-4 Seducince	15 US-IU-136-18/-8 Sequence	12 US-IU-138-187-29 Sequence	1/ US-10-850-8/3-4 Sequence	17 US-10-850-873-8 Sequence	17 US-10-850-873-29 Sequence	15 US-10-282-122A-47524 Sequence	14 US-10-126-845-104 Sequence	17 US-10-955-656-104 Sequence	15 US-10-259-194A-216 Sequence	16 US-10-437-963-115028 Sequence	13 IIG-10-116-289-4	13 US-10-116-288-4 Sequence	17 US-10-634-645-4 Sequence	13 US-10-116-288-5 Sequence	14 US-10-126-845-15 Sequence	14 US-10-126-845-73 Semience	בין מנו מין	15 US-10-116-275-103 Sequence	16 US-10-764-235-15 Sequence	7-742-645-F	מילות מילו מילו מילו מילו מילו מילו מילו מילו	17 US-10-955-656-15 Seguence	17 US-10-955-656-73 Seguence	9 US-09-789-836-12 Semience 1	27 200 000 000 000 000 000 000 000 000 0	9 US-09-785-802A-10 Seguence 1	10 US-09-997-465B-4 Sequence	13 IIG-10-116-288-1	13 US-IU-II6-288-I Sequence	14 US-10-226-956-286 Sequence	14 TO-10-000 - 000 000 000 000 000 000 000 00	14 US-10-0//-555-1 Sequence	14 US-10-211-088-304 Sequence	14 US-10-156-570A-27 Sequence	14 US-10-126-845-1 Sequence	1 110-10-136-845-14 September 2	DOMESTICATION AT THE PART OF T	Ta OS-TO-170-040-To	14 US-10-126-845-72 Sequence	14 US-10-126-845-74 Sequence	15 US-10-136-187-1 Sequence	15 US-10-116-275-102 Semience	. 000000000 POT-101-01-01-01-01	13 03-10-110-2/3-104 3educince	בין ספל דיד סדר סדר מדי	15 US-10-361-208-4/3 Sequence	15 US-10-232-410-2 Sequence	15 US-10-416-285-1 Sequence	16 US-10-764-235-1 Sequence	16 US-10-764-235-14 Sequence	16 US-10-764-235-16 Sequence	16 US-10-764-235-59 Sequence	16 US-10-751-380-8 Semience	17 TIG-10-706-739-1	יייי בייייייי פרי בייייייי פרי פרי פרי פרי פרי פרי פרי פרי	T - C2-T0-820-8/3-T	17 US-10-634-645-1 Sequence	17 US-10-795-081A-9 Sequence	17 US-10-823-259-38 Semience	17 11S-10-803-054-38 Segmente	17 00-10-027-23-10 00 00-11 01 01 01 01 01 01 01 01 01 01 01 01 0	17 00-10-902-903-01 0-01-01-01-01-01-01-01-01-01-01-01-01-01	T OS-TO-SOS TO SEGUENCE	17 US-10-955-656-14 Sequence	17 US-10-955-656-16 Sequence	17 US-10-955-656-72 Sequence	17 US-10-955-656-74 Sequence	14 US-10-013-815-20 Sequence	14 US-10-126-845-6 Sequence	14 US-10-128-843-6 Sequence	14 US-10-126-845-64 Sequence 64, A	15 HS-10-116-275-94 Semience 94 A
1.8 14 16 US-10-764-235-58 Sequence 1.8 14 17 US-10-955-656-7 Sequence 1.8 14 17 US-10-955-656-65 Sequence 1.8 16 14 US-10-126-845-5 Sequence 1.8	.8 16 14 US-10-126-845-63 Sequence	1.8 16 15 US-10-116-275-93 Sequence	1.8 16 17 US-10-955-656-5 Sequence	1.8 16 17 US-10-955-656-63 Seguence	1.8 18 16 US-10-784-309A-1 Sequence	1.8 18 16 US-10-784-309A-2 Sequence	on To	0.5 IS IS US-IU-136-18/-8 sequence	0.5 15 15 US-IU-136-18/-29 Sequence	0.5 IS I US-IU-850-8/3-4 Sequence	0.5 15 17 US-10-850-873-8 Sequence	0.5 15 17 US-10-850-873-29 Sequence	0.5 365 15 US-10-282-122A-47524 Sequence	7.9 17 14 US-10-126-845-104 Sequence	7.9 17 17 US-10-955-656-104 Sequence	7.9 802 15 US-10-259-194A-216 Sequence	7.9 802 16 US-10-437-963-115028 Sequence	6 4 10 13 TG-10-116-288-4	b.b IU I3 US-IU-IIb-288-4 Sequence	6.6 10 17 US-10-634-645-4 Sequence	6.6 11 13 US-10-116-288-5 Sequence (	6.6 11 14 US-10-126-845-15 Seguence	6.6 11 14 US-10-126-845-73 Semience	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	6.6 11 15 US-10-116-275-103 Sequence	6.6 11 16 US-10-764-235-15 Seguence	6 6 11 17 TIS-10-634-645-5	יייייייייייייייייייייייייייייייייייייי	6.6 11 17 US-10-955-656-15 Sequence	6.6 11 17 US-10-955-656-73 Sequence	6.6 12 9 US-09-789-836-12 Semience 13		6.6 12 9 US-U9-785-802A-10 Sequence 1	6.6 12 10 US-09-997-465B-4 Sequence	- Section 11 13 11 11 11 11 11 11 11 11 11 11 11	6.6 12 13 US-IU-II6-288-I Sequence	6.6 12 14 US-10-226-956-286 Sequence		6.6 IZ I4 US-IU-U/-555-I Sequence	6.6 12 14 US-10-211-088-304 Sequence	6.6 12 14 US-10-156-570A-27 Sequence	6.6 12 14 US-10-126-845-1 Seguence	. 6246men 2 12 17 11 11 11 17 17 17 17 17 17 17 17 17	Transport of the control of the cont	oco or sequence	6.6 12 14 US-10-126-845-72 sequence	6.6 12 14 US-10-126-845-74 Sequence	6.6 12 15 US-10-136-187-1 Sequence	6.6 12 15 tts-10-116-275-102 Segmence		0:0 TS TS 03-T0-TT0-Z\3-T0\ 0:0 TS		Sequence 201-201-208-4/3 Sequence	6.6 12 15 US-10-232-410-2 Sequence	6.6 12 15 US-10-416-285-1 Sequence	6.6 12 16 US-10-764-235-1 Sequence	6.6 12 16 US-10-764-235-14 Sequence	6.6 12 16 US-10-764-235-16 Sequence	6.6 12 16 US-10-764-235-59 Seguence	6.6 12 16 US-10-751-380-8 Semience	1-851-301-01-311 tr cr 3-3	1	8:6 IZ I/ US-10-820-8/3-1 Sedneuce	6.6 12 17 US-10-634-645-1 Sequence	6.6 12 17 US-10-795-081A-9 Sequence	6.6 12 17 US-10-823-259-38 Segmente	6 6 12 17 115-10-823-254-38 Semience	00000000 00 TT TO	0.0 IZ I/ 00-10-90Z-933-31 0-00 I/ 01 00 00-00-00 00 00-00-00 00-00-00 00-00-	oce It In Court and It of the State of the S	6.6 12 17 US-10-955-656-14 Sequence	6.6 12 17 US-10-955-656-16 Sequence	6.6 12 17 US-10-955-656-72 Sequence	6.6 12 17 US-10-955-656-74 Sequence	6.6 13 14 US-10-013-815-20 Sequence	6.6 13 14 US-10-126-845-6 Sequence	0.0 IS IN US-IU-120-843-0 Sequence	6.6 13 14 US-10-126-845-64 Sequence 64, A	6 6 13 15 118-10-116-275-94
7 61.8 14 16 US-10-764-215-58 Sequence 7 61.8 14 17 US-10-955-656-7 Sequence 7 61.8 14 17 US-10-955-656-65 Sequence 7 61.8 16 14 US-10-126-845-5 Sequence 9	61.8 16 14 US-10-126-845-63 Sequence	7 61.8 16 15 US-10-116-275-93 Sequence	7 61.8 16 17 US-10-955-656-5 Sequence	7 61.8 16 17 US-10-955-656-63 Sequence	7 61.8 18 16 US-10-784-309A-1 Sequence	7 61.8 18 16 US-10-784-309A-2 Sequence	Parameter and the contract of	6 60.5 IS IS US-IU-I36-I8/-8 Sequence	6 60.5 15 15 08-10-138-18/-29 Sequence	6 50.5 15 1/ US-IU-850-8/3-4 Sequence	6 60.5 15 17 US-10-850-873-8 Sequence	6 60.5 15 17 US-10-850-873-29 Sequence	6 60.5 365 15 US-10-282-122A-47524 Sequence	4 57.9 17 14 US-10-126-845-104 Sequence	4 57.9 17 17 US-10-955-656-104 Sequence	4 57.9 802 15 US-10-259-194A-216 Sequence	4 57.9 802 16 US-10-437-963-115028 Seguence	2 55 5 10 13 112 112 12 14 15 15 15 15 15 15 15 15 15 15 15 15 15	36.6 10 13 0S-10-116-Z88-4 Sequence	3 56.6 10 17 US-10-634-645-4 Sequence	3 56.6 11 13 US-10-116-288-5 Sequence	3 56.6 11 14 US-10-126-845-15 Seguence	3 56.6 11 14 US-10-126-845-73 Sequence	0. 111111111111111111111111111111111111	3 56.6 11 15 US-10-116-275-103 Sequence	3 56.6 11 16 US-10-764-235-15 Sequence	3 56 K 11 17 118-10-634-645-5	מייניים אייניים אייניי	3 56.6 11 17 US-10-955-656-15 Sequence	3 56.6 11 17 US-10-955-656-73 Sequence	3 56.6 12 9 US-09-789-836-12 Semience 13	THE PROPERTY OF THE PROPERTY O	3 56.6 12 9 US-09-785-802A-10 Sequence 1	3 56.6 12 10 US-09-997-465B-4 Sequence	3 F F F 12 11 11 11 11 Common 3	3 56.6 12 13 US-10-116-288-1 Sequence	3 56.6 12 14 US-10-226-956-286 Sequence	0.000 11 11 11 11 11 10 10 10 10 00 00 00	3 56.6 IZ 14 0S-10-0/1-555-1 Sequence	3 56.6 12 14 US-10-211-088-304 Sequence	3 56.6 12 14 US-10-156-570A-27 Sequence	3 56.6 12 14 US-10-126-845-1 Sequence	2 EE E 12 14 172-124-124 COMMONDER		30:00 TZ T4 02-10-120-043-10 Sedueitce	3 56.6 12 14 US-10-126-845-72 Sequence	3 56.6 12 14 US-10-126-845-74 Sequence	3 56.6 12 15 US-10-136-187-1 Sequence	3 56.6 12 15 HS-10-116-275-102 Semience	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	00-10-10-10-10-10-10-10-10-10-10-10-10-1		3 20.6 12 15 US-1U-301-4/3 Sequence	3 56.6 12 15 US-10-232-410-2 Sequence	3 56.6 12 15 US-10-416-285-1 Sequence	3 56.6 12 16 US-10-764-235-1 Sequence	3 56.6 12 16 US-10-764-235-14 Sequence	3 56.6 12 16 US-10-764-235-16 Sequence	3 56.6 12 16 US-10-764-235-59 Sequence	3 56.6 12 16 US-10-751-380-8 Semience	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TOTAL COLUMN TO THE TAX TO THE TA	see it in the second seed the	3 56.6 12 17 US-10-634-645-1 Sequence	3 56.6 12 17 US-10-795-081A-9 Sequence	3 56.6 12 17 US-10-823-259-38 Semience	2 55 5 12 17 115-10-823-25 36 Semience		0 00.00 IL II 00-10-302-31 0-00-00-00-00-00-00-00-00-00-00-00-00-0	מפקתמות מולי בי	3 56.6 12 17 US-10-955-656-14 Sequence	3 56.6 12 17 US-10-955-656-16 Sequence	3 56.6 12 17 US-10-955-656-72 Seguence	3 56.6 12 17 US-10-955-656-74 Sequence	3 56.6 13 14 US-10-013-815-20 Sequence	3 56.6 13 14 US-10-126-845-6 Sequence	5 55.6 15 14 US-10-120-643-6 Sequence	3 56.6 13 14 US-10-126-845-64 Sequence 64, A	3 56 6 12 15 115-116-275-94 Semience 94 D

489, A 484, A 284, A 155447 133086 81, Ap 981, Ap 247339 168365 26, Ap	000000000000000000000000000000000000000	Sequence 61877, A Sequence 61877, A Sequence 17859, Sequence 16924, Sequence 129795, Sequence 129795, Sequence 281, Appl Sequen	4004170070 40007000000000000000000000000	1126 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Sequence 118, App Sequence 120, App Sequence 124, App Sequence 124, App Sequence 126, App Sequence 136, App Sequence 137, App Sequence 137, App Sequence 136, App Sequence 136, App Sequence 136, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 138, App Sequence 131, App Sequence 131, App Sequence 131, App
15 US-10- 10 US-09- 16 US-10- 16 US-10- 19 US-10- 15 US-10- 15 US-10- 16 US-10- 14 US-10- 14 US-10-	15 US-10- 15 US-10- 15 US-10- 15 US-10- 16 US-10- 16 US-10- 16 US-10- 16 US-10- 16 US-10-	15 US-10- 16 US-10- 15 US-10- 16 US-10- 16 US-10- 14 US-10- 10 US-09- 16 US-09- 16 US-09- 16 US-09- 16 US-09- 16 US-09-	15 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	15 88-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-116 188-10-10	15 08-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-10-115 18-
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US-10-937-758A-121 US-10-424-599-148890 US-10-437-963-186113 US-10-369-493-23251	US-10-425-114-72928 US-10-425-114-51856	US-10-437-963-127459 US-10-282-122A-68759	US-10-437-963-142252 US-10-156-761-8243	US-10-425-114-43299 US-10-425-114-56873	US-10-425-114-71723 US-10-369-493-17549	US-10-437-963-136158 HS-10-156-761-13178	US-10-173-999-44	US-10-399-405-3 US-10-684-206-12	US-10-156-761-11800 US-10-369-493-3486	US-10-369-493-20003	US-10-282-122A-6191/ US-10-238-075-614	US-10-437-963-132188	US-10-732-923-14404	US-10-732-923-1801 US-10-732-923-1812	US-10-437-963-131683	US-10-756-761-12207	US-10-732-923-13939 US-10-425-114-63755	US-10-425-114-63781	US-10-424-599-215078	US-10-424-599-208110	US-10-369-493-18389	US-10-149-310-40 US-10-732-923-13942	US-10-437-963-181649 US-10-437-963-152789	US-10-437-963-182576	US-10-004-3/8A-14 US-10-936-626-101	US-10-938-061-101 US-10-295-027-1193	US-10-936-626-100	US-10-938-061-100 US-10-104-047-2283	US-10-648-593-139	US-10-369-493-5031	US-10-373-801-22 HS-10-437-963-132501	US-10-449-831A-57	US-10-449-831A-63 US-10-282-122A-52567	US-10-116-288-2	US-10-126-845-18 US-10-126-845-76	US-10-116-275-106	US-10-764-235-18 US-10-634-645-2	US-10-955-656-18	US-10-955-656-76 US-10-116-288-8	US-10-126-845-9 US-10-126-845-20
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			Sequence	Sequence	Sequence	Sequence	Seguence	Sequence 36	Sequence 84	Sequence 84	Sequence 36	Sequence 84	Sednence 36	Sequence 84	Sequence 36	Sequence 84	Sequence 84	Sequence 84	Sequence 84	Sequence 84	Sequence 84	Sequence 84	Sequence 84	Sequence 84	Sequence 84	Sequence 36	Sequence 34	Sequence 360 Sequence 280	Sequence 84	Sequence 84,	Sequence 36	Sequence 84	Sequence 6,	Sequence 1,	Sequence 8	Sequence	Sequence	Sequence 1	Sequence 37 Sequence 14	Sequence 3
US-10-227-874-84 US-10-227-876-84 US-10-227-878-84 US-10-229-974-84	0-230-024-84 0-230-113-84	0-230-183-84 0-230-234-84	0-230-426-84 Sequence	J-230-427-84 Sequence J-230-433-84 Sequence	3-230-435-84 Sequence 3-230-438-84 Sequence	0-232-222-84 Sequence	0-223-088-366 Sequence	7-223-090-366 Sequence 360-219-070-84 Sequence 84	7-219-472-84 Sequence 84. 7-219-527-84 Sequence 84.	3-227-877-84 Sequence 84	J-223-087-366 Sequence 36(	0-216-166-84 Sequence 84	223-089-366 Sequence 36	J-216-163-84 Sequence 84 J-418-064-2 Sequence 2,	3-223-081-36 Sequence 36	0-219-063-84 Sequence 84	7-219-066-84 Sequence 84 7-219-067-84 Sequence 84	0-219-068-84 Sequence 84	0-219-073-84 Sequence 84	0-219-440-84 Sequence 84,	0-219-525-84 Sequence 84	7-219-526-84 Sequence 84 7-219-530-84 Sequence 84	0-219-531-84 Sequence 84,	2-219-533-84 Sequence 84	7-230-437-84 Sequence 84.	)-223-082-366 Sequence 36( )-174-364-6 Semience 6.	0-174-364-34 Sequence 34	7-305-654-366 Sequence 36()-080-334-289 Sequence 28()	3-232-226-84 Sequence 84,	7-230-130-84 Sequence 84,	0-081-056-366 Sequence 360	0-232-230-84 Sequence 84	7-246-583-6 Sequence 6, 7-246-583-34 Sequence 34	0-311-129-1 Sequence 1,	7-119-480-84 Sequence 8 7-689-832-6 Sequence 6	3-689-832-34 Sequence	0-425-114-59211 Sequence 5	US-10-437-963-132627 Sequence 1	S-09-870-759-37 S-09-870-759-144 Sequence 14	9-751-708A-37 Sequence 3
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7.4 304 14 US-1 7.4 304 14 US-1 7.4 304 14 US-1 7.4 304 14 US-1	7.4 304 14 US-10-230-024-84 7.4 304 14 US-10-230-113-84	7.4 304 14 US-10-230-183-84 7.4 304 14 US-10-230-234-84	7.4 304 14 US-10-230-426-84 Sequence	7.4 304 14 US-10-230-427-84 Sequence 7.4 304 14 US-10-230-433-84 Sequence	7.4 304 14 US-10-230-435-84 Sequence 7.4 304 14 US-10-230-438-84 Sequence	7.4 304 14 US-10-232-284 Sequence 7.4 304 14 US-10-223-084-366 Sequence	7.4 304 14 US-10-223-088-366 Sequence	7.4 304 14 US-10-219-070-84 Sequence 84,	7.4 304 14 US-10-219-472-84 Sequence 84, 7.4 304 14 US-10-219-527-84 Sequence 84,	7.4 304 14 US-10-227-877-84 Sequence 84	7.4 304 14 US-10-223-087-366 Sequence 360 7.4 304 14 US-10-223-083-366 Sequence 360	7.4 304 14 US-10-216-166-84 Sequence 84	7.4 304 14 US-10-223-089-366 Sequence 36	7.4 304 14 US-10-216-163-84 Sequence 84 7.4 304 14 US-10-418-064-2 Sequence 2,	7.4 304 14 US-10-223-081-366 Sequence 36	7.4 304 14 US-10-219-063-84 Sequence 84	7.4 304 14 US-10-219-066-84 Sequence 84, 7.4 304 14 US-10-219-067-84 Sequence 84,	7.4 304 14 US-10-219-068-84 Sequence 84	7.4 304 14 US-10-219-073-84 Sequence 84 Se	7.4 304 14 US-10-219-480-84 Sequence 84,	7.4 304 14 US-10-219-525-84 Sequence 84	7.4 304 14 US-10-219-526-84 Sequence 84, 7.4 304 14 US-10-219-530-84 Sequence 84,	7.4 304 14 US-10-219-531-84 Sequence 84, 7.4 304 14 US-10-219-532-84 Semience 84,	7.4 304 14 US-10-219-533-84 Sequence 84	7.4 304 14 US-10-230-437-84 Sequence 84, 7.4 304 14 US-10-232-228-84 Sequence 84,	7.4 304 14 US-10-223-082-366 Sequence 36 7.4 304 15 US-10-174-364-6 Sequence 6.	7.4 304 15 US-10-174-364-34 Sequence 34	7.4 304 15 US-10-3US-654-366 Sequence 36 7.4 304 15 US-10-080-334-289 Sequence 28	7.4 304 15 US-10-232-226-84 Sequence 84,	7.4 304 15 US-10-230-130-84 Sequence 84	7.4 304 15 US-10-081-056-366 Sequence 36(	7.4 304 15 US-10-232-230-84 Sequence 84	7.4 304 15 US-10-246-583-6 Sequence 6, 7.4 304 15 US-10-246-583-34 Sequence 34,	7.4 304 15 US-10-311-129-1 Sequence 1,	4 304 15 US-10-119-480-84 Sequence 8 4 304 16 US-10-689-832-6 Sequence 6	7.4 304 16 US-10-689-832-34 Sequence	7.4 305 15 US-10-425-114-59211 Sequence 5	327 16 US-10-437-963-132627 Sequence 1	7.4 352 9 US-09-870-759-37 Sequence 37 7.4 352 9 US-09-870-759-144 Sequence 14	7.4 352 10 US-09-751-708A-37 Sequence 37.4 352 10 US-09-751-708A-144 Sequence 1
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Sequence 114067,
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Sequence 68640, A
Sequence 226794,
Sequence 33065, A
Sequence 44299, A
Sequence 152339,
 Sequence 24, Application US/10126845

Sequence 24, Application US/10126845

Publication No. US20030181367A1

GENERAL INFORMATION:

APPLICANT: Lambkin, Imelda J.

APPLICANT: Lambkin, Imelda J.

APPLICANT: Pinilla, Clemencia

APPLICANT: Houghten, Clemencia

APPLICANT: Houghten, WEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

TITLE OF INVERTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

TITLE OF INVERTION: WIGHER, US/10/126,845

CURRENT PLING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 119

SEQ ID NO 24

LENGTH: 17
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 Sequence 32, Application US/10126845

Sequence 32, Application US/10126845

Publication No. US20030181367A1

GENERAL INFORMATION:

APPLICANT: Lambkin, Imelda J.

APPLICANT: Lambkin, Imelda J.

APPLICANT: Houghten, Richard

TITLE OF INVENTION: MEMBRANG TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

TITLE OF INVENTION: MEMBRANG TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

CURRENT PILING DATE: 2002-10-15

CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 119

SEQ ID NOS: 119

SEQ ID NO 92

SEQ ID NOS: 13
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 Length 17;
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US-10-425-114-6640
US-10-424-599-226794
US-10-425-114-39065
US-10-425-114-39065
US-10-421-114-39065
US-10-424-599-152339
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 ; OTHER INFORMATION: membrane translocating peptide US-10-126-845-24
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 NAME/KEY: MISC_FEATURE

LOCATION: (1)...(17)

OTHER INFORMATION: D form amino acid
US-10-126-845-82
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Best Local Similarity
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 JS-10-126-845-24
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Sequence 182201,
Sequence 121323,
Sequence 377, App
Sequence 2501, Ap
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Sequence 54208, A
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1 US-10-126-845-78

US-10-116-275-97

US-10-116-275-108

US-10-116-275-108

US-10-16-235-20

US-10-16-235-20

US-10-16-235-20

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US-10-955-99

US-10-955-9
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: O'Mahony, Daniel J.

APPLICANT: Lambkin, Inmelda J.

APPLICANT: Lambkin, Inmelda J.

APPLICANT: Lambkin, Inmelda J.

TITLE OF INVENTION: CONUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY

TITLE OF INVENTION: CONUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY

TITLE OF INVENTION: AGENTS.

CURRENT APPLICATION NUMBER: 10/126,845

FRIOR APPLICATION NUMBER: 10/126,845

PRIOR APPLICATION NUMBER: 09/671,089

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 1999-09-27

PRIOR APPLICATION NUMBER: 60/156,246

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 119

SOSTWARE: PATENTIN VEFSION 3.1
 Sequence 82, Application US/10955656

| Sequence 82, Application US/10955656
| Publication No. US20050101762A1
| GENERAL INFORMATION:
| APPLICANT: O'Mahony, Daniel J.
| APPLICANT: Infland J.
| APPLICANT: Pinilla, Clemencia
| APPLICANT: Pinilla, Clemencia
| APPLICANT: Houghten, Richard
| TITLE OF INVENTION: COUNTGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
| TITLE OF INVENTION: COUNTGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
| TITLE OF INVENTION: AGENTS
| TITLE OF INVENTION: AGENTS
| TITLE OF INVENTION: AGENTS
| FILE REFERENCE: PAG. 481-4 USA
| CURRENT APPLICATION NUMBER: US/10/26,845
| PRIOR APPLICATION NUMBER: 09/671,089
| PRIOR PELING DATE: 2000-09-27
| PRIOR APPLICATION NUMBER: 06/156,246
| PRIOR APPLICATION NUMBER: 06/156,246
| NUMBER OF SEQ ID NOS: 119
| SOFTWARE: PATENTING DATE: 2000-09-27
| NUMBER OF SEQ ID NOS: 119
| SOFTWARE: PATENTING DATE: 2000-09-27
| TENCOR APPLICATION NUMBER: 06/156,246
| NUMBER OF SEQ ID NOS: 119
| SOFTWARE: PATENTING DATE: 2000-09-27
| TENCOR APPLICATION NUMBER: 06/156,246
| TENCOR APPLICATION NUMBER: 06/1
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 Length 17;
 Indels
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100.0%; Score 76; DB 17;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 17; Conservative 0; Mismatches 0;
 i OTHER INFORMATION: membrane translocating peptide
US-10-955-656-24
 RESULT 5
US-10-955-656-24
Sequence 24, Application US/10955656
Publication No. US20050101762A1
 FEATURE:
OTHER INFORMATION: D form peptide
FEATURE:
1 KKKRKAAAAVLLPVLLA 17
 1 KKKRKAAAAVLLPVLLA 17
 1 KKKRKAAAAVLLPVLLA 17
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 SEQ ID NO 24
 TYPE: PRT
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 US-10-116-275-112

Sequence 112, Application US/10116275

Sequence 112, Application US/10116275

Publication No. US20030211476A1

GENERAL INFORMATION:

APPLICANT: Brayden, David

APPLICANT: Brayden, David

APPLICANT: Higgins, Lisa

APPLICANT: Higgins, Lisa

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and Methods and

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors

FILE REPRENCE: ELGO7/20087

CURRENT APPLICATION NUMBER: US/10/116,275

CURRENT APPLICATION NUMBER: US/10/116,275

CURRENT PILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 349

SOFTWARE: PatentIn version 3.1

SEQ ID NO 112

LENGTH: 17
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US-10-116-275-112
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 Sequence 24, Application US/10764235

Sequence 24, Application US/10764235

Publication No. US20040138132A1

GENERAL INFORMATION:

APPLICANT: O'Mahony, Daniel J.

APPLICANT: Lambkin, Imelda J.

TITLE OF INVENTION: MEMBEANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

FILE REFERENCE: P26,479-B USA

CURRENT APPLICATION NUMBER: US/10/764,235

CURRENT FILING DATE: 2004-01-23

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 1999-09-27

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patentin version 3.1

SEQ ID NO 24

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Matches 17; Conservative 0; Mismatches 0; Indels
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 OTHER INFORMATION: membrane translocating peptide
Mismatches
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ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
17; Conservative
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NAME/KEY: MISC FEATURE

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Best Local Similarity
 FEATURE:
NAME/KEY: VARIANT
LOCATION: 1
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US-10-955-656-108
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 US-10-136-187-30

US-10-136-187-30

US-10-136-187-30

Publication No. US20030203865A1

GENERAL INFORMATION:

APPLICANT: Paul, Raiph

APPLICANT: Cudmore, Sally

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

FILE REFERENCE: 2267206330

CURRENT APPLICATION NUMBER: US/10/136,187

CURRENT APPLICATION NUMBER: US 60/287,786

PRIOR FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 30

LENGTH. 17

LENGTH. 17
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 Sequence 30, Application US/10850873
; Sequence 30, Application US/10850873
; Publication No. US20050025821A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Cudmore, Sally
; APPLICANT: Cudmore, Sally
; APPLICANT: Cudmore, Sally
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
; FILE REFERENCE: 22672005300
; CURRENT APPLICATION NUMBER: US/10/850,873
; CURRENT FILING DATE: 2004-05-20
; PRIOR FILING DATE: 2004-04-30
; PRIOR FILING DATE: 2001-04-30
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
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86.7%; Pred. No. 0.028;
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Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 17; Conservative 0; Mismatches 0;
 LOCATION: 1; COTHER INFORMATION: Lysine is attached to dansyl US-10-136-187-30
 OTHER INFORMATION: Synthetic Construct
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i OTHER INFORMATION: D form amino acid
US-10-955-656-82
 1 KKKRKAAAAVLLPVLLA 17
 1 KKKRKAAAAVLLPVLLA 17
 ORGANISM: Artificial Sequence
 |:| |||||||||||
1 KKKKAAAVLLPVLLA 15
 3 KRKAAAAVLLPVLLA 17
 Query Match 76.3%
Best Local Similarity 86.7%
Matches 13, Conservative
 NAME/KEY: VARIANT
 10-850-873-30
 TYPE: PRT
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Sequence 108, Application US/10955656

Publication No. US20050101762A1

GENERAL INFORMATION:
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Inclarda J.
APPLICANT: Houghten, Richard
TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
TITLE OF INVENTION: AGENTS
TITLE APPLICANT: LAGRENCE: P.56, 481-A USA
CURRENT APPLICATION NUMBER: US/10/955,656
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 VS-10-126-845-108

Sequence 108, Application US/10126845

Publication No. US20030181367A1

GENERAL INFORMATION:

APPLICANT: O'Mahony, Daniel J.

APPLICANT: Lambini, Inelda J.

APPLICANT: Houghten, Richard

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

FILE REFERENCE: E1067/20058

CURRENT APPLICATION NUMBER: US/10/126,845

CURRENT FILING DATE: 2002-10-15
 Gaps
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 ;
0
 FEATURE:
OTHER INFORMATION: D-form peptide; Comprises opioid peptide
 Score 58; DB 17; Length 17;
Pred. No. 0.028;
 73.7%; Score 56; DB 14; Length 19; 92.9%; Pred. No. 0.063;
 1; Indels
 ; OTHER INFORMATION: Lysine is attached to dansyl US-10-850-873-30
 Query Match 76.3%; Score 58; DB Best Local Similarity 86.7%; Pred. No. 0.02 Matches 13; Conservative 1; Mismatches
 0; Mismatches
 FEATURE:
OTHER INFORMATION: Synthetic Construct
 LOCATION: (1). (19)
OTHER INFORMATION: D-form amino acid
 NUMBER OF SEQ ID NOS: 119
SOFTWARE: PatentIn version 3.1
 TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
 ; NAME/KEY: MOD RES
; LOCATION: (19)...(19);
; OTHER INFORMATION: Amidation
US-10-126-845-108
 |:| ||||||||||||
1 KKKXAAAVLLPVLLA 15
 3 KRKAAAAVLLPVLLA 17
 4 RKAAAAVLLPVLLA 17
 4 RKKAAAVLLPVLLA 17
 13; Conservative
 NAME/KEY: MISC_FEATURE
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 Sequence 106, Application US/10126845

Publication No. US20030181367A1

GENERAL INFORMATION,

APPLICANT: O'Mahony, Daniel J.

APPLICANT: Dimbkin, Imelda J.

APPLICANT: Pinilla, Clemencia

APPLICANT: Pinilla, Clemencia

APPLICANT: Pinilla, Richard

ITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

FILE REPERBENCE: B1067/20058

CURRENT APPLICATION NUMBER: US/10/126,845

CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 119

SOFTWARE: ParentIn version 3.1

SEQ ID NO 106

LENGTH: 20
 Gaps
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 FEATURE:
OTHER INFORMATION: D-form peptide; Comprises opioid peptide
 PEATURE:
OTHER INFORMATION: D-form peptide; Comprises opioid peptide
 Score 56; DB 17; Length 19;
Pred. No. 0.063;
0; Mismatches 1; Indels
 Query Match 72.4%; Score 55; DB 14; Length 20; Best Local Similarity 80.0%; Pred. No. 0.096; Matches 12; Conservative 2; Mismatches 1; Indels
PRIOR APPLICATION NUMBER: 10/126,845
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 09/671,089
PRIOR APPLICATION NUMBER: 09/156,246
PRIOR PILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 119
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 108
LENGTH: 19
TAVED: ---
 LOCATION: (1). (19)
OTHER INFORMATION: D-form amino acid
 NAME/KEY: MISC_FEATURE
LOCATION: (1). \(\tilde{(1)}\) (20)
OTHER INFORMATION: D-form amino acid
 TYPE: PRT ORGANISM: Artificial Sequence
 TYPE: PRT ORGANISM: Artificial Sequence
 Query Match 73.7%;
Best Local Similarity 92.9%;
Matches 13; Conservative
 NAME/KEY: MOD RES
LOCATION: (19).
COTHER INFORMATION: Amidation
US-10-955-656-108
 FEATURE:
NAME/KEY: MOD RES
LOCATION: (20)...(20)
OTHER INPORMATION: Amidation
US-10-126-845-106
 3 KRKAAAAVLLPVLLA 17
 4 RKKAAAVLLPVLLA 17
 NAME/KEY: MISC FEATURE LOCATION: (1)..(19)
 RESULT 11
US-10-126-845-106
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Sequence 106, Application US/10955656

Publication No. US20050101762A1

GENERAL INFORMATION:

APPLICANT: O'Mahony, Daniel J.

APPLICANT: O'Mahony, Daniel J.

APPLICANT: Dembkin, Imelda J.

APPLICANT: Dembkin, Imelda J.

APPLICANT: Houghten, Richard

ITILE OF INVENTION: AGENTS OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY

ITILE OF INVENTION: AGENTS

TITLE OF INVENTION: AGENTS

TITLE OF INVENTION: AGENTS

TITLE OF INVENTION: AGENTS

PLICE REPRENEES: D204-09-30

CURRENT APPLICATION NUMBER: US/10/955,656

CURRENT APPLICATION NUMBER: 09/671,089

PRIOR FILING DATE: 2000-09-27

PRIOR PILING DATE: 1999-09-27

PRIOR PILING DATE: 1999-09-27

PRIOR PILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 119

SEQ ID NO 106

LENGTH: 20

MANDER: DEMORTH: 20
 Sequence 124, Application US/10126103

Publication No. US20030224486A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICATION: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB PATHWA

FILE REFERENCE: D0108-IND

CURRENT PELING DATE: 2002-04-19

FRIOR PELING DATE: 2001-04-19

PRIOR PELING DATE: 2001-04-19

PRIOR PELING DATE: 2001-04-26

PRIOR PELING DATE: 2001-04-26

PRIOR PELING DATE: 2001-04-26

PRIOR PELING DATE: 2001-04-26

PRIOR PELING DATE: 2001-04-16

SOFTWARE: PRECENTION NUMBER: US 60/346,986

PRIOR FILING DATE: 2002-01-09

SOFTWARE: PRECENTION VORTER OF SEQUID NO SEQUID NO 124

SEQUID NO 124

LENGTH: 29
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 Gaps
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 OTHER INFORMATION: D-form peptide; Comprises opioid peptide
 DB 17; Length 20
 1; Indels
 72.4%; Score 55; DB 17;
80.0%; Pred. No. 0.096;
tive 2; Mismatches
 , OTHER INFORMATION: Synthetic peptide sequence.
US-10-126-103-124
 NAME/KEY: MISC_FEATURE
LOCATION: (1). \(^{20}\)
OTHER INFORMATION: D-form amino acid
 TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
 ORGANISM: Artificial Sequence
 NAME/KEY: MOD RES
LOCATION: (20)...(20)
CTHER INFORMATION: Amidation
US-10-955-656-106
 3 KRKAAAAVLLPVLLA 17
 Query Match
Best Local Similarity 80.04
Matches 12; Conservative
JS-10-955-656-106
 US-10-126-103-124
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 US-10-126-845-48

| Sequence 40, Application US/10126845
| Sequence 40, No. US20030181367A1
| Publication No. US20030181367A1
| GENERAL INFORMATION:
| APPLICANT: Lambkin, Immeda J.
| APPLICANT: Lambkin, Immeda J.
| APPLICANT: Pinilla, Clemencia | APPLICANT: Pinilla DATE: 2002-10-15 | UNBER OF SEQ ID NOS: 119 | SOFTWARE: Patentin version 3.1 | SEQ ID NO 48
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 Gaps
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 Sequence 3, Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:

APPLICANT: Paul, Ralph

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Sally

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

FILE REFERENCE: 226272005300

CURRENT APPLICATION NUMBER: US/10/136,187

CURRENT FILING DATE: 2001-04-30

PRIOR FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 3

LENGTH: 16
 OTHER INFORMATION: dansylated membrane translocating peptide
 Score 53; DB 14; Length 16;
Pred. No. 0.16;
 DB 15; Length 16;
 1; Indels
 1; Indels
 Score 53; DB 1:
Pred. No. 0.16;
 Query Match 69.7%; Score 53; DB Best Local Similarity 85.7%; Pred. No. 0.16 Matches 12; Conservative 1; Mismatches
 1; Mismatches
 ; OTHER INFORMATION: Synthetic Construct US-10-136-187-3
 1 KKKRKAAAAVLLP-VLLA 17
 2 KKKRKVAAVALLPAVLLA 19
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 LOCATION: (1)...(1)
OTHER INFORMATION: dansylated
 Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
 4 RKAAAAVLLPVLLA 17
 1 KKKAAAVLLPVLLA 14
 4 RKAAAAVLLPVLLA 17
 NAME/KEY: MOD RES
 US-10-126-845-48
 FEATURE:
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 US-10-858-367-60
Sequence 60, Application US/10858367
Sequence 60, Application US/10858367
Sequence 60, Application US. US20050026191A1
Sequence 60, Application US. US20050026191A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb
TILE REFERENCE: DO1006NP
FILE REFERENCE: DO306NP
CURRENT APPLICATION NUMBER: US/10/858,367
CURRENT APPLICATION NUMBER: 60/475,234
PRIOR FILING DATE: 2003-06-02
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 29
 Sequence 124, Application US/10431096

Sequence 124, Application US/10431096

Bublication No. US20040086896A1

GENERAL INFORMATION:
APPLICANT: Bristol—Wers Squibb Company
TITLE OF INVENTION: PATHWAY
TITLE OF INVENTION: PATHWAY

FILE REFERENCE: D0108A C1P
CURRENT FILING DATE: 2003-05-07

PRIOR PILING DATE: 2003-05-07

PRIOR PLING DATE: 2001-04-19

PRIOR FILING DATE: 2002-04-19

SPIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2002-04-19

SOUTHWARE: PARE SOUTH ON NUMBER: US 60/286,645

PRIOR FILING DATE: 2002-04-19

SOUTHWARE: PARE SOUTH ON
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 Gaps
 1;
 1,
 70.4%; Score 53.5; DB 17; Length 29; 77.8%; Pred. No. 0.24; tive 0; Mismatches 3; Indels 1
 Length 29;
 Length 29;
 Indels
 Indels
Score 53.5; DB 15;
Pred. No. 0.24;
0; Mismatches 3;
 Match 70.4%; Score 53.5; DB 15; Local Similarity 77.8%; Pred. No. 0.24; les 14; Conservative 0; Mismatches 3;
 ; OTHER INFORMATION: Synthetic peptide sequence. US-10-431-096-124
 ; OTHER INFORMATION: Synthesized Peptide US-10-858-367-60
 2 KKKRKVAAVALLPAVLLA 19
 1 KKKRKAAAAVLLP-VLLA 17
 2 KKKRKVAAVALLPAVLLA 19
 1 KKKRKAAAAVLLP-VLLA 17
Query Match
Best Local Similarity 77.8%;
Matches 14; Conservative
 Query Match
Best Local Similarity 77.8
Matches 14; Conservative
 ORGANISM: Artificial
 ORGANISM: Artificial
 RESULT 14
US-10-431-096-124
 Query Match
 Best Loc
Matches
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; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance U; OTHER INFORMATION: take Across the GIT" US-10-116-275-91
 APPLICANT: Byrne, Daragha APPLICANT: Byrne, Daragha APPLICANT: Lambkin, Imelda APPLICANT: Lambkin, Imelda APPLICANT: Lambkin, Imelda APPLICANT: Lambkin, Lisa TPLICANT: Higgins, Lisa TPLICANT: Higgins, Lisa TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cell Receptors TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors FILE REFERENCE: BIO NUMBER: US/10/116,275
CURRENT APPLICATION WHOMER: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: Patentin version 3.1
SEQ ID NO 91
LENGTH: 16
 Sequence 3, Application US/10764235
| Sequence 3, Application US/10764235
| Publication No. US20040138132A1
| GENERAL INFORMATION;
| APPLICANT: O'MAHONION;
| APPLICANT: C'MAHONION;
| TITILE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
| FILE REFERENCE: P26,479-B USA
| CURRENT FILING DATE: 2004-01-23
| FRIOR APPLICATION NUMBER: 09/671,089
| FRIOR APPLICATION NUMBER: 60/156,246
| FRIOR APPLICATION NUMBER: 60/156,246
| FRIOR PILING DATE: 1999-09-27
| WINBER OF SEQ ID NOS: 59
| WINBER OF SEQ ID NOS: 59
| CONTUMARE: Patentin version 3.1
 Gaps
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 69.7%; Score 53; DB 15; Length 16;
85.7%; Pred. No. 0.16;
 Score 53; DB 16; Length 16;
Pred. No. 0.16;
1; Mismatches 1; Indels
 69.7%; Score 53; DB 15; Length 16; 85.7%; Pred. No. 0.16;
 Indels
 Indels
 , OTHER INFORMATION: membrane translocating peptide US-10-764-235-3
 1; Mismatches
 Sequence 91, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: 0. Mahony, Daniel J.
APPLICANT: Brayden, David
 TYPE: PRT
ORGANISM: Artificial Sequence
 69.7%;
 TYPE: PRT
ORGANISM: Artificial Sequence
 4 RKAAAAVLLPVLLA 17
 :| ||||||||||||
1 KKKAAAVLLPVLLA 14
 4 RKAAAAVLLPVLLA 17
 Query Match
Best Local Similarity 85.7
Matches 12; Conservative
 Best Local Similarity 85.7
Matches 12, Conservative
 Query Match 69.7
Best Local Similarity 85.7
Matches 12; Conservative
 US-10-116-275-91
 US-10-764-235-3
 SEQ ID NO 3
LENGTH: 16
 Query Match
 RESULT 20
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 Sequence 7, Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:
APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Paul, Ralph
APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 226272005300
CURRENT APPLICATION NUMBER: US/10/136,187

CURRENT FILING DATE: 2002-09-13

PRIOR FILING DATE: 2001-04-30
 Score 53; DB 15; Length 16;
Pred. No. 0.16;
 1; Indels
 ; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to galactose
US-10-136-187-7
 ; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to dansyl
US-10-136-187-28
 1; Mismatches
 NUMBER OF SEQ ID NOS: 45
SOFTHARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 16
 OTHER INFORMATION: Synthetic Construct
 FEATURE:
OTHER INFORMATION: Synthetic Construct
 69.7%;
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
4 RKAAAAVLLPVLLA 17
 Query Match 69.77
Best Local Similarity 85.77
Matches 12, Conservative
 FEATURE: NAME/KEY: VARIANT
 NAME/KEY: VARIANT
 US-10-136-187-28
 RESULT 18
US-10-136-187-7
 TYPE: PRT
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 RESULT 25
US-10-850-873-28
US-10-850-873-28
; Sequence 28, Application US/10850873
; Publication No. US2085082181
; GENERAL INFORMATION:
 APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahony, Daniel J
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: LADD METHODS FOR THEIR PRODUCTION
; FILE REFERENCE: 226272005300
; CURRENT FILING DATE: 2004-05-20
; PRIOR FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 16
 Sequence 7, Application US/10850873

Bublication No. US20050025821A1

Bublication No. US20050025821A1

GABRERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Daniel J.

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

FILE REFERENCE: 22627205300

CURRENT FILING DATE: 2004-05-20

CURRENT FILING DATE: 2004-06-30

PRIOR PILING DATE: 2001-04-30

PRIOR FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE FREISE FREISE FOR Windows Version 4.0
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 Score 53; DB 17; Length 16;
Pred. No. 0.16;
 Indels
 1; Indels
 ; OTHER INFORMATION: Lysine is attached to galactose US-10-850-873-7
 Pred. No. 0.16
1; Mismatches
 1; Mismatches
 OTHER INFORMATION: Synthetic Construct
 ORGANISM: Artificial Sequence
Best Local Similarity 85.7%;
Matches 12; Conservative
 Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
 ORGANISM: Artificial Sequence
 4 RKAAAAVLLPVLLA 17
 4 RKAAAAVLLPVLLA 17
 NAME/KEY: VARIANT
 US-10-850-873-7
 LENGTH: 16
 SEQ ID NO 7
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 US-10-764-235-48

Sequence 48, Application US/10764235

Publication No. US20040138132A1

APPLICANT: O'Mahony, Daniel J.

APPLICANT: O'Mahony, Daniel J.

APPLICANT: O'Mahony, Daniel J.

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

TITLE OF INVENTION: WEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

TITLE OF INVENTION: WEMBRANE US/10/764,235

CURRENT FILING DATE: 2004-01-23

PRIOR FILING DATE: 2006-09-27

PRIOR PELING DATE: 1999-09-27

PRIOR FILING DATE: 1999-09-27

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PATENTI Nersion 3.1

SEQ ID NO 48

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial Sequence
 Gaps
 ;
 APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Paul, Ralph
APPLICANT: Cudmore, Sally
APPLICANT: Cudmore, Sally
APPLICANT: Co'Mahony, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REPRENCE: 226272065300
CURRENT APPLICATION NUMBER: US/10/850,873
CURRENT PLING DATE: 2004-05-20
PRIOR PLING DATE: 2002-04-30
PRIOR PLING DATE: 2002-04-30
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FRESER FOR WINDOWS Version 4.0
 OTHER INFORMATION: dansylated membrane translocating peptide
 DB 16; Length 16;
 Length 16;
 1; Indels
 DB 17;
 Score 53; DB 1
Pred. No. 0.16;
1; Mismatches
 69.7%; Score 53;
) OTHER INFORMATION: Synthetic Construct
US-10-850-873-3
 Sequence 3, Application US/10850873 Publication No. US20050025821A1 GENERAL INFORMATION:
 TYPE: PRT ORGANISM: Artificial Sequence
 ; LOCATION: (1)...(1); OTHER INFORMATION: dansylated US-10-764-235-48
 Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
 4 RKAAAAVLLPVLLA 17
 RKAAAAVLLPVLLA 17
 1 KKKAAAVLLPVLLA 14
 FEATURE:
NAME/KEY: MOD_RES
 US-10-850-873-3
 SEQ ID NO 3
LENGTH: 16
 Query Match
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 Gaps
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 Sequence 9, Application US/10136187;
Publication No. US20030203865A1;
GENERAL INFORMATION:
APPLICANT: Harvie, Pierrot
APPLICANT: Harvie, Pierrot
APPLICANT: Cudmore, Sally
APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES;
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 226272005300
CURRENT FILING DATE: 2002-09-13
FRIOR APPLICATION NUMBER: US/10/136,187
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PASESEQ for Windows Version 4.0
LENGTH: 20
 APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Cudmore, Sally
APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 226272005300
 Length 20;
 DB 15; Length 20;
 Indels
 ; OTHER INFORMATION: Lysine is attached to galactose US-10-136-187-9
 Score 53; DB 15;
Pred. No. 0.2;
 1; Mismatches
 1; Mismatches
 NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
 Score 53;
Pred. No.
 CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US 60/287,786
PRIOR FILING DATE: 2001-04-30
 ; OTHER INFORMATION: Synthetic Construct US-10-136-187-5
 FEATURE: OTHER INFORMATION: Synthetic Construct
 US-10-850-873-5; Sequence 5. Application US/10850873; Publication No. US20050025821A1; GENERAL INFORMATION:
 TYPE: PRT ORGANISM: Artificial Sequence
 69.7%;
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match 69.7%;
Best Local Similarity 85.7%;
Matches 12, Conservative
 4 RKAAAAVULLPVLLA 17
 4 RKAAAAVLLPVLLA 17
 1 KKKAAAVLLPVLLA 14
 Best Local Similarity 85.7
Matches 12; Conservative
 NAME/KEY: VARIANT
 Query Match
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 Sequence 48, Application US/10955656
Publication No. US20050101762A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Houghten, Richard
TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARWACEUTICALLY
TITLE OF INVENTION: AGENTS
FILE REFERENCE: P26,481-A USA
CURRENT APPLICATION NUMBER: US/10/955,656
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: 10/126,845
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 119
SOUTHWARE: PATENTIN VERSION 3.1
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0
 OTHER INFORMATION: dansylated membrane translocating peptide
 US-10-136-187-5

Sequence 5, Application US/10136187

Sequence 5, Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Sally

APPLICANT: O'MADONY, Daniel J.

IITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

IITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
 Score 53; DB 17; Length 16; Pred. No. 0.16;
 DB 17; Length 16;
 1; Indels
 1; Indels
 ; OTHER INFORMATION: Lysine is attached to dansyl US-10-850-873-28
 Score 53; DB 17
Pred. No. 0.16;
 1; Mismatches
 Mismatches
 FILE REFERENCE: 226272005300
CURRENT APPLICATION NUMBER: US/10/136,187
FEATURE:
OTHER INFORMATION: Synthetic Construct
 69.7%;
 TYPE: PRT
ORGANISM: Artificial Sequence
 NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: dansylated
US-10-955-656-48
 69.7%;
 4 RKAAAAVLLPVLLA 17
 Query Match
Best Local Similarity 85.74
Conservative
 Query Match 69.7
Best Local Similarity 85.7
Matches 12; Conservative
 FEATURE:
NAME/KEY: VARIANT
 LOCATION:
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ALFLICANT: FINITIA, Clemencia
ALFLICANT: Houghten, Richard
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20058
CURRENT APPLICATION NUMBER: US/10/126,845
CURRENT PILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin version 3.1
SEQ ID NO 109
LEMETH: 21
TYPE
 Sequence 111, Application US/10126845
Publication No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: O'Mahony, Daniel J.
APPLICANT: I cambkin, Imelda J.
APPLICANT: Finilla, Clemencia
APPLICANT: Finilla, Clemencia
APPLICANT: Finilla, Clemencia
APPLICANT: Houghten, Richard
ITILE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REPERENCE: E1067/20058
CURRENT PILING DATE: 2002-10-15
CURRENT DATE: 2002-10-15
 Gaps
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 DB 14; Length 21; 0.21;
 69.7%; Score 53; DB 14; Length 21;
 1; Indels
 1; Mismatches
 FEATURE:
OTHER INFORMATION: Comprises opioid peptide
 OTHER INFORMATION: Comprises opioid peptide
 Score 53;
Pred. No.
 NAME/KEY: MISC_FEATURE
LOCATION: (1)._(1)
OTHER INFORMATION: Linked to biotin-LC
 NAME/KEY: MISC_FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: Linked to biotin-LC
PEATURE:
 LOCATION: (18)...(21)
OTHER INFORMATION: D-form amino acid
 LOCATION: (2). (21)
OTHER INFORMATION: D-form amino acid
 TYPE: PRT
ORGANISM: Artificial Sequence
 69.7%;
85.7%;
 ORGANISM: Artificial Sequence
 NAME/KEY: MOD RES
LOCATION: (21)...(21)
COTHER INFORMATION: Amidation
US-10-126-845-109
 NAME/KEY: MOD RES
LOCATION: (21√..(21)
OTHER INFORMATION: Amidation
 4 RKAAAAVLLPVLLA 17
 Query Match
Best Local Similarity 85.7%
 NAME/KEY: MISC_FEATURE
 NAME/KEY: MISC_FEATURE
 US-10-126-845-111
 US-10-126-845-111
 Query Match
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 Gaps
 US-10-20-4/3-9

Sequence 9, Application US/10850873

Publication No. US2050025821A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: O'Mahony, Daniel J.

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISE: US/10/10850,873

CURRENT FILING DATE: 2004-05-20

PRIOR APPLICATION NUMBER: US 60/287,786

PRIOR PILING DATE: 2001-04-30

PRIOR PILING DATE: 2001-04-30

PRIOR PILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 9

LENGTH: 20

LENGTH: 20

LENGTH: 20
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 69.7%; Score 53; DB 17; Length 20;
85.7%; Pred. No. 0.2;
tive 1; Mismatches 1; Indels
 Score 53; DB 17; Length 20;
Pred. No. 0.2;
 Indels
 LOCATION: 1
COTHER INFORMATION: Lysine is attached to galactose US-10-850-873-9
 1; Mismatches
 CURRENT APPLICATION NUMBER: US/10/850,873
CURRENT FILING DATE: 2004-05-20
PRIOR APPLICATION NUMBER: US/10/136,187
PRIOR PILING DATE: 2002-04-30
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
TYPE: PRI
 OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
 Sequence 109, Application US/10126845
Publication No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: O'MANONY, Daniel J.
APPLICANT: Lambkin, Imelda J.
 69.7%;
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 4 RKAAAAVLLPVLLA 17
 4 RKAAAAVLLPVLLA 17
 Query Match
Best Local Similarity 85.74
Matches 12; Conservative
 Query Match
Best Local Similarity 85.73
Matches 12; Conservative
 NAME/KEY: VARIANT
 -10-126-845-109
 US-10-850-873-5
 RESULT 31
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Sequence 2, Application US/10126845

Fublication No. US20030181367A1

GENERAL INFORMATION:

APPLICANT: O'Mahony, Daniel J.

APPLICANT: Lambkin, Imelda J.

APPLICANT: Pinilla, Clemencia

APPLICANT: Pinilla, Clemencia

APPLICANT: Pinilla, Clemencia

APPLICANT: Houghten, Richard

TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM

FILE REFERENCE: E1067/20058

CURRENT APPLICATION NUMBER: US/10/126,845

CURRENT APPLICATION NUMBER: US/10/126,845

CURRENT APPLICATION NUMBER: US/10/126,845

SOFTWARE: Patentin version 3.1

SEQ ID NO 2.

LENGTH: 15
 Gaps
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 Ouery Match 67.1%; Score 51; DB 14; Length 15; Best Local Similarity 92.3%; Pred. No. 0.3; Matches 12; Conservative 0; Mismatches 1; Indels
 DB 17; Length 21;
 ; OTHER INFORMATION: membrane translocating peptide US-10-126-845-2
 FEATURE:
OTHER INFORMATION: Comprises opioid peptide FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Linked to biotin-LC
 1; Mismatches
 69.7%; Score 53;
85.7%; Pred. No.
 PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 09/671,089
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/156,246
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin version 3.1
SEQ ID NO 111
 LOCATION: (2). 7(21)
OTHER INFORMATION: D-form amino acid
 PRIOR APPLICATION NUMBER: 10/126,845
 ; Sequence 3, Application US/10126845; Publication No. US20030181367A1
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 NAME/KEY: MOD RES
LOCATION: (21)..(21)
OTHER INFORMATION: Amidation
 4 RKAAAAVLLPVLLA 17
 12; Conservative
 S KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 NAME/KEY: MISC FEATURE LOCATION: (2)...(21)
 Best Local Similarity
Matches 12; Conserva
 US-10-955-656-111
 RESULT 36
US-10-126-845-3
 Query Match
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 Sequence 109, Application US/10955656

Publication No. US20050101762A1

GENERAL INFORMATION:

APPLICANT: Lambkin, Inmelda J.

APPLICANT: Houghen, Richard

TITLE OF INVENTION: CONUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY

TITLE OF INVENTION: AGENTS

FILE REPRENCE: P25, 481-A USA

CURRENT APPLICATION NUMBER: US/10/955,656

CURRENT FILING DATE: 2004-09-30

PRIOR PILING DATE: 2004-09-30

PRIOR PILING DATE: 2006-09-27

PRIOR FILING DATE: 2006-09-27

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 119

SEQ ID NO 109

SEQ ID NO 109
 Sequence 111, Application US/10955656
Publication No. US20050101762A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: O'MAHONY, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Danilla, Clemencia
APPLICANT: Pinilla, Clemencia
APPLICANT: HOUGHERS OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
TITLE OF INVENTION: AGENTS
FILE REFERENCE: P26,481-A US/
CURRENT APPLICANT WIMBER: US/10/955,656
CURRENT FILING DATE: 2004-09-30
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 Gaps
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 Score 53; DB 17; Length 21;
Pred. No. 0.21;
 1; Indels
 1; Indels
 Pred. No. 0.21;
1; Mismatches
 1; Mismatches
 OTHER INFORMATION: Comprises opicid peptide
 NAME/KEY: MISC FEATURE
LOCATION: (1)._(1)
OTHER INFORMATION: Linked to biotin-LC
 LOCATION: (18) .. (21)
OTHER INFORMATION: D-form amino acid
 69.7%;
85.78;
 ORGANISM: Artificial Sequence
 FEATURE:

NAME/KEY: MOD RES

LOCATION: (21)...(21)

OTHER INFORMATION: Amidation
US-10-955-656-109
 4 RKAAAAVLLPVLLA 17
 4 RKAAAAVLLPVLLA 17
 Best Local Similarity 85.7
Matches 12, Conservative
 Best Local Similarity 85.7
Matches 12, Conservative
 FEATURE:
NAME/KEY: MISC_FEATURE
 RESULT 34
US-10-955-656-111
 US-10-955-656-109
 Query Match
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APPLICANT: HOUGHTEN, RICHARD
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
THE REPERENCE: E 10.67/20058
CURRENT APPLICATION NUMBER: 10.5/10/126,845
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 61
LENGTH: 15
 Gaps
 Sequence 2, Application US/10136187

Sequence 2, Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Sally

APPLICANT: O'Mahony, Daniel J.

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

CURRENT APPLICATION NUMBER: US/10/136,187

CURRENT FILING DATE: 2062-09-13

FRIOR APPLICATION NUMBER: US 60/287,786

PRIOR PILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 2

LENGTH: 15
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 Score 51; DB 15; Length 15; Pred. No. 0.3; 0; Mismatches 1; Indels
 Score 51; DB 14; Length 15;
Pred. No. 0.3;
 1; Indels
 0; Mismatches
 PEATURE:
, OTHER INFORMATION: Synthetic Construct
US-10-136-187-2
 NAME/KEY: MISC_FEATURE
1 LOCATION: (1)..(15)
2 OTHER INFORMATION: D form amino acid
US-10-126-845-61
 Sequence 6, Application US/10136187; Publication No. US20030203865A1; GENERAL INPORMATION:
APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
 FEATURE:
OTHER INFORMATION: D form peptide
O'Mahony, Daniel J.
Lambkin, Imelda J.
Pinilla, Clemencia
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 67.1%;
 Query Match 67.1%;
Best Local Similarity 92.3%;
Matches 12; Conservative
 5 KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 1 KKAAAVLLPVLLA 13
 Query Match 67.1
Best Local Similarity 92.3
Matches 12; Conservative
 RESULT 39
US-10-136-187-2
 RESULT 40
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 Sequence 60, Application US/10126845
Fublication No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: O'MAHONY,
APPLICANT: Lambkin, Imelda J.
APPLICANT: Pinilia, Clemencia
APPLICANT: Pinilia, Clemencia
APPLICANT: Pinilia, Clemencia
APPLICANT: Pinilia, Clemencia
APPLICANT: Houghten, Richard
TITLE OP INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20058
CURRENT APPLICATION UNDERS: US/10/126,845
CURRENT APPLICATION NUMBER: US/10/126,845
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SSOTHARE: Patent In version 3.1
SEQ ID NO 60
LENGTH: 15
 ö
 APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Houghten, Richard
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REPERRUCE: B1067/20058
CURRENT APPLICATION NUMBER: US/10/126,845
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 3
LENGTH: 15
 Gaps
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 67.1%; Score 51; DB 14; Length 15; 92.3%; Pred. No. 0.3;
 67.1%; Score 51; DB 14; Length 15; 92.3%; Pred. No. 0.3;
 1; Indels
 OTHER INFORMATION: membrane translocating peptide
 0; Mismatches
 0; Mismatches
 LOCATION: (1). (15)
OTHER INFORMATION: D form amino acid
) NAME/KEY: MOD_RES

; LOCATION: (15)..(15)

; OTHER INFORMATION: linked to FITC-LC

US-10-126-845-3
 ; Sequence 61, Application US/10126845; Publication No. US20030181367A1; GENERAL INFORMATION:
 OTHER INFORMATION: D form peptide
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 S KAAAAVLLPVLLA 17
 | [|||||||||
1 KKAAAVLLPVLLA 13
 5 KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 Query Match 67.1
Best Local Similarity 92.3
Matches 12; Conservative
 Best Local Similarity 92.3
Matches 12, Conservative
 NAME/KEY: MISC FEATURE
 GENERAL INFORMATION:
 US-10-126-845-60
 RESULT 38
US-10-126-845-61
 -10-126-845-60
 TYPE: PRT
 Query Match
 FEATURE:
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APPLICANT: Harvie, Pierrot
APPLICANT: Harvie, Ralph
APPLICANT: Paul, Ralph
APPLICANT: O'Mahory, Daniel
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 226272065300
CURRENT APPLICATION NUMBER: US/10/136,187
CURRENT PLING DATE: 20002-09-13
PRIOR RILING DATE: 20002-09-13
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 15
 Query Match 67.1%; Score 51; DB 15; Length 15; Best Local Similarity 92.3%; Pred. No. 0.3; Matches 12; Conservative 0; Mismatches 1; Indele
) OTHER INFORMATION: Synthetic Construct US-10-136-187-13
 Sequence 13, Application US/10136187
Publication No. US20030203865A1
GENERAL INFORMATION:
 ORGANISM: Artificial Sequence
 5 KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 TYPE: PRT
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APPLICANT: Cudmore, Sally

APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE: 226272005300
CURRENT APPLICATION NUMBER: US/10/136,187
CURRENT APPLICATION NUMBER: US 60/287,786
PRIOR PILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 15
 Sequence 12, Application US/10136187
Publication No. US20030203865A1
GENERAL INFORMATION:
APPLICANT: Harvie, Pierrot
APPLICANT: Paul, Ralph
APPLICANT: Cudmore, Sally
APPLICANT: O'Mahony, Daniel J.
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
 Score 51; DB 15; Length 15;
Pred. No. 0.3;
0; Mismatches 1; Indels
 Score 51; DB 15; Length 15;
Pred. No. 0.3;
0; Mismatches 1; Indels
 ; OTHER INFORMATION: Lygine is attached to DOPE-succinyl US-10-136-187-12
 ; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to galactose
US-10-136-187-6
 FILE REFERENCE: 226272005300

CURRENT APPLICATION NUMBER: US/10/136,187

CURRENT FILING DATE: 2002-09-13

FRIOR PILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FREESEQ for Windows Version 4.0

SERVICH: 15
 OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
 67.1%;
92.3%;
 ORGANISM: Artificial Sequence
 1 KKAAAVLLPVLLA 13
 S KAAAAVLLPVLLA 17
 Query Match 67.13
Best Local Similarity 92.33
Matches 12, Conservative
 5 KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 NAME/KEY: VARIANT LOCATION: 1
 FEATURE:
NAME/KEY: VARIANT
 TYPE: PRT
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 GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Daniel J.

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

FILE REPERENCE: 226272005300

CURRENT APPLICATION NUMBER: US 60/287,786

FRIOR APPLICATION NUMBER: US 60/287,786

FRIOR APPLICATION NUMBER: US 60/287,786

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 45
 ö
 Query Match 67.1%; Score 51; DB 15; Length 15; Best Local Similarity 92.3%; Pred. No. 0.3; Matches 12; Conservative 0; Mismatches 1; Indels
 OTHER INFORMATION: Lysine is attached to des-Proline
 ; OTHER INFORMATION: Serine is attached to galactose US-10-136-187-31
 FEATURE:
OTHER INFORMATION: Synthetic Construct
RESULT 43
US-10-136-187-31
Sequence 31, Application US/10136187
; Publication No. US20030203865A1
 ORGANISM: Artificial Sequence
 NAME/KEY: VARIANT LOCATION: 1
 NAME/KEY: VARIANT LOCATION: 15
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US-10-136-187-13

RESULT 42

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Gaps
 Gaps
 Sequence 35, Application US/10136187

Publication No. US20030203865A1

Publication No. US20030203865A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Paul, Ralph

APPLICANT: Cudmore, Sally

APPLICANT: Or INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

CURRENT APPLICATION NUMBER: US/10/136,187

CURRENT PILING DATE: 2020-09-13

PRIOR APPLICATION NUMBER: US 60/287,786

PRIOR PILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 35

LENGTH: 15
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0
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 US-10-136-187-36

| Sequence 36, Application US/10136187
| Publication No. US20030203865A1
| GENERAL INFORMATION:
| APPLICANT: Harvie, Pierrot
| APPLICANT: Paul, Ralph
| APPLICANT: Cudmore, Sally
| APPLICANT: Cudmore, Sally
| TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
| TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
| TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
| TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
| FILE REPREBRENCE: 226272065300
| CURRENT FILING DATE: 2002-09-13
 OTHER INFORMATION: Lysine is attached to Cholesteryl-succinyl
 DB 15; Length 15;
 1; Indels
 Indels
 1;
Pred. No. 0.3;
0; Mismatches
 0; Mismatches
 PRIOR APPLICATION NUMBER: US 60/287,786 PRIOR PILING DATE: 2001-04-30 NUMBER OF SEQ ID NOS: 45 SOFTWARE: PREESEQ FOR Windows Version 4.0
 LOCATION: (1)...(15)
OTHER INFORMATION: D amino acid sequence
 Score 51;
Pred. No.
 OTHER INFORMATION: Synthetic Construct
 67.18;
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
92.3%;
 1 KKAAAVLLPVLLA 13
 Query Match
Best Local Similarity 92.5
Best Local 21 Conservative
 S KAAAAVLLPVLLA 17
 5 KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
Best Local Similarity 92.3
Matches 12; Conservative
 NAME/KEY: VARIANT
 NAME/KEY: VARIANT
 RESULT 46
US-10-136-187-35
 US-10-136-187-35
 SEQ ID NO 36
LENGTH: 15
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 Gaps
 Sequence 33, Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

TITLE OF INVENTION: LIPTD-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

CURRENT APPLICATION NUMBER: US 60/287,786

PRIOR PILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 33

LENGTH: 15
 ö
 ; OTHER INFORMATION: Lysine is attached to Cholesteryl-succinyl US-10-136-187-33
 67.1%; Score 51; DB 15; Length 15;
 Length 15;
 1; Indels
 LOCATION: 1
OTHER INFORMATION: Lysine is attached to DOPE-succinyl
 Score 51; DB 15;
Pred. No. 0.3;
 0; Mismatches
 FEATURE: OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
FEATURE:
 TYPE: PRT ORGANISM: Artificial Sequence
 Query Match 67.1%;
Best Local Similarity 92.3%;
Matches 12; Conservative
 TYPE: PRT ORGANISM: Artificial Sequence
 S KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 1 KKAAAVLLPVLLA 13
 NAME/KEY: VARIANT
 NAME/KEY: VARIANT LOCATION: 1
 US-10-136-187-34
 LOCATION: 1
 Query Match
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Gaps

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Score 51; DB 15; Length 15; Pred. No. 0.3;

67.1%;

0; Mismatches

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FEATURE:

NAMEKEY: VARIANT

LOCATION: 1

OTHER INFORMATION: Lysine is attached to DSPE-PEG5K-succinyl
US-10-136-187-38
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 38 LENGTH: 15
 OTHER INFORMATION: Synthetic Construct
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 92.3
Matches 12; Conservative
 S KAAAAVLLPVLLA 17
 RESULT 50
US-10-136-187-39
 LOCATION:
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 Gaps
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 Sequence 38, Application US/10136187

Sequence 38, Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:
APPLICANT: Harvie, Pierrot
APPLICANT: Commore, Sally
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION
FILE REFERENCE 22627206340

CURRENT APPLICATION NUMBER: US/10/136,187

FRIOR APPLICATION NUMBER: US 60/287,786

PRIOR APPLICATION NUMBER: US 60/287,786

NUMBER OF SEQ ID NOS: 45
 Sequence 37, Application US/10136187

Publication No. US20030203865A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Sally

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

FILE REFERENCE: 22627206330

CURRENT FAPLICATION NUMBER: US/10/136,187

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: US 60/287,786
 ; LOCATION: 1
; OTHER INFORMATION: Lysine is attached to DSPE-PEGSK-succinyl
US-10-136-187-36
 ; OTHER INFORMATION: Lysine is attached to DMPE-PEG5K-succinyl
US-10-136-187-37
 Length 15;
 Score 51; DB 15; Length 15;
Pred. No. 0.3;
0; Mismatches 1; Indels
 1; Indels
 Score 51; DB 15;
Pred. No. 0.3;
 0; Mismatches
 NUMBER OF SEQ 1D NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 15
FEATURE:
OTHER INFORMATION: Synthetic Construct
 OTHER INFORMATION: Synthetic Construct
 Query Match 67.1%;
Best Local Similarity 92.3%;
Matches 12; Conservative
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 92.3*;
Matches 12; Conservative
 S KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 FEATURE:
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Sequence 39, Application US/10136187
; Sequence 39, Application US/10136187
; Publication No. US203030203865A1
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; APPLICANT: Paul, Ralph
; APPLICANT: Cudmore, Sally
; APPLICANT: O'Mahory, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; TITLE OF INVENTION: LIPID-COMPRISING POR THEIR PRODUCTION
; FILE REFERENCE: 226272063300
; CURRENT APPLICATION NUMBER: US/10/136,187
; CURRENT APPLICATION NUMBER: US 60/287,786
; PRIOR PILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 15
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 ; OTHER INFORMATION: Lysine is attached to DMPE-PEG5K-succinyl US-10-136-187-39
 Score 51; DB 15; Length 15;
Pred. No. 0.3;
 Mismatches
 FRATURE:
OTHER INFORMATION: Synthetic Construct
 Search completed: June 2, 2005, 01:43:52 Job time *: 103.344 secs
 TYPE: PRT ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
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 1 KKAAAVLLPVLLA 13
 NAME/KEY: VARIANT
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importin beta-1 su
probable receptor-
hypothetical prote
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 glycosyl transfera
hypothetical prote
probable acid-CoA
 hypothetical prote
 PSE1 protein - yea
hypothetical prote
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probable hemin ABC
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 cytochrome c-type
 June 2, 2005, 01:26:16; Search time 13.2812 Seconds (without alignments) 123.157 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 283416
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 í,
 Total number of hits satisfying chosen parameters:
 283416 seqs, 96216763 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 750 summaries
 OM protein - protein search, using sw model
 BLOSUM62
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 Perfect scores
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Maximum DB
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 Database
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 Result
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Cjaccession: AF3275

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, S;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes: Proc. Natl. Acad. Scl. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten: A;Reference number: AD3252; PMID:11756688

A;Status: preliminary

C,Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

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A;Genetics:
A;App position: I

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Gaps ö

Score 42; DB 2; Length 297; Pred. No. 19; 2; Mismatches 0; Indels

55.3%;

Query Match Best Local Similarity 81.8 Matches 9; Conservative

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ALIGNMENTS

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A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Naturers: Foulgar, D.; Fritz, C.; Fullia, M.; Fulliappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Frighta, M.; Fulliappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sakiguch, J.; Sakowska, A.; Saro,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguch, J.; Sato, T.; Scanlon
Akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Togonoi, J.; Yoshida, J.;
A;Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Residuse: 1-527 KUMA.
A;Residuse: 1-527 KUMA.
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C;Superfamily: phosphotransferase system glucose-specific enzyme II, factor II; phospho
 A;Cross-references: UNIPROT:P54715; GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12649
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
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Best Local Similarity 50.0
Matches 8; Conservative
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R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rlo, M.C.; Chambon, P.; Basset, P.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal ce
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submitted to the EMBL Data Library, November 1995

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 A, Accession: S78011
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 ### metalloproteinase (EC 3.4.24.-) membrane type precursor - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C;Accession: 146673
B;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, F.
Proc. Natl. Acad. Sci. U.S.A. 92, 2770-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal ce A;Reference number: 138046; MUID:95224014; PMID:7708115
A;Accession: 146673
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-582 ARES.
A;Cross-references: EMBL:X83536; NID:9804999; PIDN:CAA58520.1; PID:9805000
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; cinc; zymogen
F;1-23/Domain: aignal sequence #status predicted <PRO-F;CL-284/Domain: activation peptide #status predicted <PRO-F;21-284/Domain: matrix metalloproteinase homology <PRO-F;21-284/Domain: matrix metalloproteinase homology <PRO-F;313-504/Domain: matrix metalloproteinase homology <PRO-F;513-504/Domain: matri
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: F64580
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-528 «TOM»
A;Cross-references: UNIPROT:025230; GB:AE000563; GB:AE000511; NID:92313593; PIDN:AAD07555
C;Superfamily: Helicobacter pylori hypothetical protein HP0209
 micrix metalloproteinase 14 (EC 3.4.24..) membrane type precursor - human NiAlternate names matrix metalloproteinase MMP14; membrane type matrix metalloproteinase Cispecies: Homo sapiens (man) (1902) (2002
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 Score 41; DB 2; Length 528;
Pred. No. 48;
2; Mismatches 1; Indels
 DB 2; Length 582;
 0; Indels
 Score 41; DB
Pred. No. 52;
2; Mismatches
 2 KKRKAAAAVL---LPVL 15
 4 KKRKVAAALLKRFTLPLL 21
 53.9%;
81.8%;
 ch 53.9%;
l Similarity 61.1%;
11; Conservative 5
 Best Local Similarity 81.8
Matches 9; Conservative
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538 SAAAVVLPVLL 548
 6 AAAAVLLPVLL 16
 Local Similarity
 Query Match
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Access-references: GDB:37571; OMIM:600754
A; Map position: 14q11-14q12
A; Map position: 14q11-14q12
A; Map position: 14q11-14q12
C; Superfamily: interestital collagenase; hemopexin repeat homology; matrix metalloprotei
C; Superfamily: interestital collagenase; hemopexin repeat homology; matrix metalloprotein
C; Superfamily: interestital collagenase; predicted <21G>
C; Superfamily: interestital collagenase; predicted <21G>
C; Ag4-97/Domain: activation peptide #status predicted <81G>
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C; Ag4-97/Domain: matrix metalloproteinase homology <AMP>
C; Ag4-97/Domain: hemopexin repeat homology <ANG>
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C; Ag4-97/Domain: hemopexin repeat homology <ANG>
C; Ag4-97/Domain: transmembrane #status predicted <ANG>
C; Ag4-97/Domain: transmembrane #status predicted <ANG-P; Ag4-Sag-Psinding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F; Ag4-98/Binding site: zinc, catalytic (His) (active) #status predicted
F; Ag4-Ag4-Versine alte: Gun #status predicted
F; Ag4-Ag4-Versine alte: Gun #status predicted
F; Ag4-Osphore alte: Gun #status predicted
 A, Residues: 1-7,'S', 9-188,'R',190,'A',192-267,'K',269-272,'HY',275,'P',277-285,'KQ',288, A, Cross-references: EMBL:D26512
A, Cross-references: EMBL:D26512
F, R, Kinoshite, T.; Takino, T.; Nakayama, K.; Selki, M.
FEBS Lett. 393, 101-104, 1996
A; Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
 A;Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP) A;Reference number: S71384; WUID:96397540; PMID:8804434
 A; Residues: 1-7,'6',9-337,'K',339-582 <SEI>
A; Cross-references: BMBL:D26512; NID:9793762; PIDN:BAA05519.1; PID:9793763
R; Sato, H.; Takino, T.; Okada, Y.; Cao, J.; Shinagawa, A.; Yamamoto, E.; Seiki, M. Nature 370, 61-65, 1994
A; Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells. A; Reference number: S45341; MUID:94286011; PMID:8015608
 ö
A;Status: translated from GB/EMBL/DDBJ
A;Molcoule type: mRNA
A;Residues: 1-7,'S', 9-582 cOKA>
A;Cross-references: EMBL:X83535; NID:g804993; PIDN:CAA58519.1; PID:g804994
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 Length 582;
 matrix metalloproteinase (EC 3.4.24.-) membrane type precursor N;Alternate names: membrane-type metalloproteinase C;Species: Rattus norvegicus (Norway rat)
 Indela
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 submitted to the EMBL Data Library, January 1994
 DB
52;
 Mismatches
 Score 41;
Pred. No.
 A;Status: nucleic acid sequence not shown
 53.9%;
81.8%;
 Query Match
Best Local Similarity 81.0-
Best Local 9, Conservative
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538 SAAAVVLPVLL 548
 6 AAAAVLLPVLL 16
 A, Reference number: S78011
 A; Gene: GDB: MMP14; MT1-MMP
 A; Molecule type: protein
A; Residues: 112-116 <SAW>
 A; Molecule type: mRNA
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A; Cross-references: UNIPROT: 09PGL7; GB: AE003881; GB: AE003849; NID: 99105093; PIDN: AAF830
 A; Lross-rererences: unterwor: questions and contents are contents. A. A. C. Franco, M.
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: H83825
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <SIM>
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298 KENRKKVAALLIPATL 313
 52.6%;
 1 KKKRKAAAAVLLPVLL 16
 Best Local Similarity 75.0 Matches 9; Conservative
 6 AAAAVLLPVLLA 17
 66 ATQAVILPVLLA 77
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-534 <KUR>
 A; Accession: F90031
 A; Gene: XF0281
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 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Residues: 1-582 <RES>
A;Crosa-references: UNIPROT:Q10739; EMBL:X83537; NID:g805012; PIDN:CAA58521.1; PID:g805C
A;Accession: 161946
A;Accession: 161946
A;Accession: totaliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Crosa-references: EMBL:X91785; NID:g1001926; PIDN:CAA62897.1; PID:g1001927
C;Genetics:
 transport protein XF0281 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Al-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accesion: #83825
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 A Generi mt-mmp
C; Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C; Superfamily: interstitial collagenase; zinc; zymogen
C; Superfamily: interstitial collagenase; zinc; zymogen
C; Superfamily: matally metalloproteinase; zinc; zymogen
F; 24-97/Domain: activation peptide #status predicted <PRO>
F; 61-284/Domain: matrix metalloproteinase homology <NMP>
F; 61-284/Domain: matrix metalloproteinase homology <NMP>
F; 313-508/Domain: hemopexin repeat homology <NNA>
F; 33, 23, 243, 249/Binding site: zinc, catalytic (Cys, His, His, His, His) (inhibited) #status
F; 240/Active site: Glu #status predicted
 Cidate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26710
E;White, S.
Submitted to the EMBL Data Library, September 1998
A;Reference number: Z20255
A;Accession: T26710

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 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 184471; 161946
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset,
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A;Title: Nembrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal 4,746ference number: 138046; MUID:95224014; PMID:7708715
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 hypothetical protein Y38H6C.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 Gaps
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 Length 310;
 3; Indels
 DB 2;
 Query Match
Best Local Similarity 61.5%; Pred. No. 43;
Matches 8; Conservative 2; Mismatches
 A.Gene: CESP:Y38H6C.2
A.Map position: 5
A:Introns: 38/2; 130/2; 171/3; 209/3; 242/2
 171 KACLAILLPILTA 183
 S KAAAAVLLPVLLA 17
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538 SAAAVVLPVLL 548
 6 AAAAVLLPVLL 16
 Genetics:
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PTS system, arbutin-like IIBC component [imported] - Staphylococcus aureus (strain N315)
 A;Cross-references: UNIPROT:Q99RVO; GB:BA000018; PID:g13702123; PIDN:BAB43415.1; GSPDB:<A;Experimental source: strain N315
 A,Gene: glvC
C,Superfamily: phosphotransferase system glucose-specific enzyme II, factor II; phospho
 C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F90031
B;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R;Kuroda, M.; Ohta, T.; Wchayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
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 A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; WUID:21311952; PMID:11418146
 C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38016
 Gaps
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 importin beta-1 subunit - fission yeast (Schizosaccharomyces pombe)
 Query Match 52.6%; Score 40; DB 2; Length 534; Best Local Similarity 50.0%; Pred. No. 71; Matches 8; Conservative 3; Mismatches 5; Indels
DB 2; Length 389;
 2; Indels
Score 40; DB 2
Pred. No. 53;
1; Mismatches
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Length 162

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Score 39;
Pred. No.
 51.3%;
 51.3%;
50.0%;
 Query Match
Best Local Similarity 50.0%;
 16
 19
 REREVEABAVLVPTL 102
 1 KKKRKAAAAVLLPVL 15
 4 QRRRSSATAVLLSLL
 1 KKKRKAAAAVLLPVLL
 1 KKKRKAAAAVLLPVLL
 8; Conservative
 Query Match
Best Local Similarity 50.0
Matches 8; Conservative
 Conservative
 Query Match
Best Local Similarity
Matches 8; Conserv
 93
 A, Gene: ycf5
 Genetics:
 Matches
 RESULT 15
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 A;Accession: T38016
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Atatus: preliminary; translated from GB/EMBL/DDBJ
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-863 <OLI>
A;Residues: 1-863 <OLI>
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A;Experimental source: strain 972h-; cosmid c1B1
C;Genetics:
 RESULT 12
(S44363
Hypothetical protein ggt (imported) - Halobacterium sp. NRC-1
(Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
(Species: NRC-1)
(
 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Crose-references: UNIPROT:Q9HNES; GB:AE004437; NID:g10581552; PIDN:AAG20275.1; GSPDB:G
C;Genetics:
A;Gene: ggt
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R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, August 1995
A;Reference number: 221762
 52.6%; Score 40; DB 2; Length 980; 56.2%; Pred. No. 1.2e+02; ive 3; Mismatches 4; Indels
 Score 40; DB 2; Length 863;
Pred. No. 1.1e+02;
 1; Indels
 2; Mismatches
 ||: :||||||:
586 KKKHKYPSVLLPVLLS 601
 52.6%;
 2 KKRKAAAAVLLPVLLA 17
 :|||| :|||||
316 RAAADILPVLL 327
 Best Local Similarity 75.0
Matches 9; Conservative
 Local Similarity 56.2
 5 KAAAAVLLPVLL 16
 A; Gene: SPDB:SPAC1B1.03c
 A; Map position: 1
 Query Match
Best Local S
Matches 9
 Query Match
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chitinase (EC 3.2.1.14) III C10923 - rice
NyAlternate names: 1,4-beta-poly-N-acetylglucosaminidase; chitodextrinase; poly-beta-glu
Cispecies: Oryza ativa (rice)
Cipacies: Oryza ativa (rice)
Cipacies: Oryza ativa (rice)
Cipacession: JC5847
RiNagasaki, H.; Yamamoto, K.; Shomura, A.; Koga-Ban, Y.; Takasuga, A.; Yano, M.; Minobe,
DNA Res. 4, 379-385, 1997
A;Title: Rice class III chitinase homologues isolated by random cloning of rice cDNAs.
A;Reference number: JC5847
A;Accession: JC5847
A;Accession: JC5847
A;Status: nucleic acid sequence not shown
A;Residues: 1-304 cNAG>
 A,Cross-references: UNIPROT:Q9SXX2; UNIPROT:O49830; DDBJ:D55714; NID:g2696232; PIDN:BAA2
C;Comment: This protein hydrohyzes poly-beta-1,4-N-acetyl glucosamine (chitin), and acts
C;Superfamily: plant chitinase III
C;Keywords: glycosidase; hydrolase III
C;Keywords: glycosidase; hydrolase III C10923 1 #status predicted <MAT>
F;155/Active site: Asp #status predicted
 C;Accession: S78242
R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Preier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensi
A;Reference number: S78238
A;Accession: S78242
 A;Cross-references: UNIPROT:P49523; EMBL:Z67753; NID:g1185127; PIDN:CAA91615.1; PID:g118
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
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 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-312 <KOW>
 Cytochrome c-type synthesis protein homolog - Odontella sinensis chloroplast N;Alternate names: hypothetical protein 312 C;Species: chloroplast Odontella sinensis C;Decies: chloroplast Odontella sinensis C;Date: 17-reb-1998 #sequence_revision 26-Feb-1998 #text_change 09-Jul-2004 C;Accession: S78242
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 Length 304;
 Length 312;
 3; Indels
 6; Indels
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 A;Genome: chloroplast
C;Superfamily: cytochrome c-type synthesis protein
C;Keywords: chloroplast
 DB (
 Score 39; DB 2
Pred. No. 63;
2; Mismatches
DB 34;
 Score 39; DB
Pred. No. 61;
 Mismatches
 4; Mismatches
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A,Molecule type: DNA
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A,Residues: 1-1089 <CON>
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A,Cross-references: UNIPROT: P32337; EMBL: Z49212; NID: 9798940; PID: 9798950; MIPS: YMR308c
R,Chow, T.Y.K.; Ash, J.; Dignard, D.; Thomas, D.Y.
R;Chow, T.Y.K.; Ash, J.; Dignard, D.; Thomas, D.Y.
A,Description: Screening and identification of a gene, PSB-1, that affects protein secription: Screening and identification of a gene, PSB-1, that affects protein secriptions: S20189
 hypothetical protein T1008.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Bocies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000
B;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K submitted to the Protein Sequence Database, March 2000
A;Reference number: 224486
A;Reference number: 224486
A;Accession: T48162
A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-1467 - GBV)
A;Cross-references: UNIPROT:Q9M033; EMBL;All61746
A;Reperimental source: cultivar Columbia; BAC clone T1008
C;Genetics:
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 PSEI protein - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein YM952.10c; protein YMR308c
C;Species: Saccharomyces cerevisiae
C;Daces 08-Jul.1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S53978; S20189
R;Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53969
A;Reference number: S53969
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A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: fadD2
C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
C;Keywords: acid-thiol ligase
F;107-557/Domain: acetate-CoA ligase homology <ACL>
 51.3%; Score 39; DB 2; Length 1089; 53.8%; Pred. No. 2e+02; ive 4; Mismatches 2; Indels
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Best Local Similarity 43.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 6; Mismatches 3; Indels
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A;Cross-references: EMBL:Z11538; NID:g4245; PID:g4246
 A;Cross-references: SGD:S0004925; MIPS:YMR308c
 304 EKHKATSMVVVPVMLS 319
 2 KKRKAAAAVLLPVLLA 17
 C; Keywords: transmembrane protein
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718 RAAGATLIPILLS 730
 S KAAAAVLLPVLLA 17
 Best Local Similarity 53.8
Matches 7; Conservative
 A; Accession: S20189
 A; Map position: 13R
 A, Gene: SGD: PSE1
 Query Match
 C, Genetics:
 RESULT 18
 RESULT 19
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 Glycosyl transferase family protein CC2077 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87506
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzbarg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87506
A;Status: preliminary
A;Anleule type: DNA
 A;Residues: Ī-318 <STO>
A;Cross-references: UNIPROT:Q9A6L6; GB:AE005673; NID:g13423558; PIDN:AAK24048.1; GSPDB:G
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A;Gene: CC2077
 A;Residues: 1-560 <COL>
A;Cross-references: UNIPROT:P95227; GB:Z86089; GB:AL123456; NID:g3261711; PIDN:CAB06682.
 Ficole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Sajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature. 393, 537-544, 1998

A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70508; MUID:98295987; PMID:9634230

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA
 probable acid-CoA ligase (EC 6.2.1.-) fadD2 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C;Accession: A70628
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Cibate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
Cibate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
Cibaccesion: T42653
Ribloccker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, November 1999
A:Reference number: Z22230
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 Length 437;
 2; Length 318;
 Indels
 3; Indels
 A, Cross-references: UNIPROT: Q9UPC5, EMBL: AL133050
A, Experimental source: adult testis; clone DKFZp434F2015
 hypothetical protein DKFZp434F2015.1 - human (fragment)
 DB 2;
86;
 DB
64;
 S1.3%; Score 39; DB ilarity 66.7%; Pred. No. 86; Conservative 3; Mismatches
 Mismatches
 Score 39;
Pred. No.
 9
 ::||| | :| |:||:
276 RRRKALALLLAPLILS 291
 2 KKRKAAAAVLLPVLLA 17
 51.3%;
ilarity 43.8%;
Conservative
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424 KKKKRAAALVL 435
 1 KKKRKAAAAVLL 12
 Query Match
Best Local Similarity
7; Conserva
 Query Match
Best Local Similarity
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 A; Accession: T42653
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-437 < AAA>
 A; Note: DKFZp434F2015.1
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C;Genetics:
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Rifeldelberg J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
I. R.R.; Mekalanos, J.J.; Vonter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
ArTitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; WUID:20406833; PMID:10952301
A;Reterine preliminary
A;Residues: 1-57.-4HIS
A;Residues: 1-58.-4HIS
A;Residues: 1-58.-4HI
A;Map position: 5
A;Introns: 68/2; 121/3; 152/3; 178/1; 234/2; 291/3; 331/3; 516/3; 698/3; 721/3; 760/3;
 hypothetical protein VCA0973 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
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 Species: Vibrio cholerae
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
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 DB 2; Length 1467
 Score 38; DB 2; Length 57; Pred. No. 19;
 Indels
 1; Mismatches
 240 KKRPAYCGRILPVLLS 255
 2 KKRKAAAAVLLPVLLA 17
 50.0%;
 Best Local Similarity 56.2
Matches 9; Conservative
 Query Match
Best Local Similarity 72.7
Matches 8; Conservative
 1 KKKRKAAAAVL 11
 34 KKKKKAAGTVL 44
 A; Note: T1008.110
 A;Gene: VCA0973
A;Map position: 2
 Query Match
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G33572
B;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bı
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J. Lory, S.; Olson, M.V.
Asture 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <STO>
A;Cross-references: UNIPROT:Q215V8; GB:AE004494; GB:AE004091; NID:g9946446; PIDN:AAG0396
 C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: A12391
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Cross-references: UNIPROT:Q8YN81; GB:BA000019; PIDN:BAB76388.1; PID:g17133826; GSPDB:CA;Experimental source: strain PCC 7120
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Reference number: A59328
A;Reference number: A59328
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamlly: Escherichia coli ribosomal protein S21
 30S ribosomal protein S21 PA0579 [imported] - Pseudomonas aeruginosa (strain PAO1)
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 hypothetical protein all4689 [imported] - Nostoc sp. (strain PCC 7120)
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 Score 38; DB 2; Length 71;
Pred. No. 23;
2; Mismatches 0; Indels
 Length 169;
 Length
 A;Gene: al14689
C;Superfamily: Synechocystis hypothetical protein slr0695
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 DB 2;
 A,Gene: rpsU; PA0579
C,Superfamily: Bscherichia coli ribosomal protein
 50.0%; Score 38; DB
80.0%; Pred. No. 23;
cive 2; Mismatches
 Query Match 50.0%; Score 38; DB Best Local Similarity 60.0%; Pred. No. 52; Matches 9; Conservative 2; Mismatches
 50.0%;
ilarity 80.0%;
Conservative 2
 A;Experimental source: strain PAO1
 8; Conservative
 1 KKKRKAAAAV 10
 23
 1 KKKRKAAAAV 10
 ERKRKAAAAV
 Query Match
Best Local Similarity
Matches 8; Conserv
 Local Similarity
nes 8; Conserv
 A;Residues: 1-169 <KUR>
 A;Status: preliminary
A;Molecule type: DNA
 A; Accession: AI2391
 44
 Query Match
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 256, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
 A,Accession: H75376
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Rosidues: 1-411 (WHI>
A,FCross-references: UNIPROT:Q9RU03; GB:AE002003; GB:AE000513; NID:g6459358; PIDN:AAF1111
A,Experimental source: strain R1
 P.R.; He
Holroyd
 A; Cross-references: UNIPROT: Q9CD27; GB: AL450380; NID: g13093799; PIDN: CAC32077.1; GSPDB: (C; Genetics:
 hypothetical protein T12H17.60 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (CjSpecies: Arabidopsis thaliana (mouse-ear cress) (CjAces: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 (CjAcession: T04562 (CjAcession: T04562 (CjAcession: Hilbert, H.; Braun, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft A;Reference number: Z15377 (A)Accession: T04562
 acyleck synthase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87227
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; F.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyć eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; SA;Title: Massive gene decay in the leprosy bacillus.
A;Authors: Preliminary
A;Accession: G87227
A;Accession: G87227
A;Accession: C87227
A;Acsidues: 1-548 <5TO>A;Acsidues: 1-54
 A;Residues: 1-627 <BEV>
A;Cross-references: UNIPROT:049648; EMBL:AL021635
A;Cross-references: UNIPROT:049648; EMBL:AL021635
C;Genetimental source: cultivar Columbia; BAC clone T12H17
C;Genetion: 4
A;Map position: 4
A;Introns: 12/1; 111/1; 144/3; 272/2; 290/3; 342/3; 399/1; 420/3; 467/3; 506/3; 531/1;
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 A;Gene: fadD2
C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
 Length 411;
 Score 38; DB 2; Length 548; Pred. No. 1.6e+02;
 Indels
 50.0%; Score 38; DB 2; I 60.0%; Pred. No. 1.2e+02; iive 2; Mismatches 4;
 6; Mismatches
 :| :| | |::||:|
289 EKHQATAMVVVPVMLS 304
 50.0%;
 2 KKRKAAAAVLLPVLLA 17
 3 KRKAAAAVILLPVILLA 17
 Query Match
Best Local Similarity 43.8
Matches 7; Conservative
 Conservative
 Query Match
Best Local Similarity
Matches 9; Conserv
 A; Molecule type: DNA
 A; Map position: 1
 C;Genetics:
A;Gene: DR1594
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 hypothetical protein F7K2.250 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05461
R;Bevan, M.; Wadler, H.; Mambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuelle submitted to the Protein Sequence Database, November 1998
A;Reference number: 215416
A;Accession: T05461
A;Molecule type: DNA
A;Residues: 1-287 <BEV.
A;Cross-references: EMBL:AL033545
A;Experimental source: cultivar Columbia; BAC clone F7K2
 Ayfitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A,Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75619
A;Accession: DROUTORY, G9RZU6; GB:AE001826; NID:G6460827; PIDN:AAF12576.1; PID:G646
A;Cocas-references: UNIPROT:Q9RZU6; GB:AE001826; NID:G6460827; PIDN:AAF12576.1; PID:G646
A;Gene: DR0015
 probable hemin ABC transporter, permease protein - Deinococcus radiodurans (strain R1) C; Species: Deinococcus radiodurans C; Species: Deinococcus radiodurans C; Species: Oa. Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C; Accession: G75619 R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.; Science 286, 1571-1577, 1999
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 hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: H75376
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 Length 354;
 Length 287;
 4; Indels
 DB 2;
85;
 S0.0%; Score 38; DB 2;
illarity 50.0%; Pred. No. 1e+02;
Conservative 4; Mismatches
 A;Map position: megaplasmid
A;Genome: plasmid
A;Note: plasmid MP1
C;Superfamily: vitamin B12 transport protein btuC
 Mismatches
 50.0%; Score 38; 60.0%; Pred. No.
 A,Map position: 4
A;Introns: 113/1; 146/3; 212/3; 269/2
A;Note: F7K2.250
 1 KKKRKAAAAVLLPVLL 16
:: | | : | | : | | | 39
4 QRSRAALSLVLLPLLL 29
 :|||| ||| : ||
135 EKKRKEEAAVAMGVL 149
 1 KKKRKAAAAVLLPVL 15
 KKRKAAAAVLLPVLL 16
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RSRILAAVLLSVLL 19
 Conservative
 Query Match
Best Local Similarity
Matches 8; Conserv
 Best Local Similarity
Matches 9; Conserv
 Query Match
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A;Cross-references: UNIPROT:Q18749; EMBL:Z70750; PIDN:CAA94750.1; GSPDB:GN00023; CESP:F2 A;Experimental source: clone C50F4
R;Gardner, A.
Bubmitted to the EMBL Data Library, April 1996
A;Reference number: Z19406
A;Accession: T21324
 A;Introns: 25/3; 47/2; 199/1; 242/1; 315/2; 544/3; 600/1; 626/1; 646/1; 666/3; 706/3; 75
 hypothetical protein KIAA0423 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00057
R;IshiKawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima, N.; Tanaka, A., submitted to the EMBL Data Library, October 1997
A;Referring to the EMBL Data Library, October 1997
A;Referring number: Z14082
A;Accession: T00057
 A;Residues: 1-1696 <ISH>
A;Cross-references: UNIPROT:Q9Y4F4; EMBL:AB007883; NID:d1179759; PIDN:BAA24853.1; PID:d1
 glycerol dehydrogenase homolog lmol737 [imported] - Listeria monocytogenes (strain EGD-¢ C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004 C;Accession: AI1291
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 A;Molecule type: DNA
A;Residues: 1-901 <WI2>
A;Cross-references: EMBL:270752; PIDN:CAA94758.1; GSPDB:GN00023; CESP:F25B3.1
A;Experimental source: clone F25B3
 Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Accession: T20122; T21324
 Gaps
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 Length 1696;
 Length 901;
 50.0%; Score 38; DB 2; Length 901 68.8%; Pred. No. 2.5e+02; Artive 0; Mismatches 5; Indels
 Indels
 Score 38; DB 2; Lei
Pred. No. 4.5e+02;
4; Mismatches 1;
 hypothetical protein F25B3.1 - Caenorhabditis elegans
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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 submitted to the EMBL Data Library, April 1996
A;Reference number: 219225
A;Accession: T20122
 108 KGKRKAIAAVPLNVRL 123
 1 KKKRKAAAAVLLPVLL 16
 50.0%;
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207 RASTALLLPILL 218
 11; Conservative
 Conservative
 S KAAAAVLLPVLL 16
 A;Experimental source: brain C;Genetics:
 Query Match
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 Query Match
Best Local Similarity
 A; Gene: CESP: F25B3.1
 A; Note: KIAA0423
 A; Map position:
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 hypothetical protein AT4903760 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Reb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: F85047
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: F85047
A;Accession: Af4013050
A;Accession: Ar4903760
A;Accession: A4403760
A;Amp position: 4
 A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Molecule type: DNA
A/Rossidues: 1.722 <SCH>
A/Kross-references: UNIPROT:Q10668; EMBL:X93590; PIDN:CAA63788.1
A/Kross-references: UNIPROT:Q10668; EMBL:X93590; PIDN:CAA63788.1
A/Kross-reference strain L972
A/Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
A/Reference number: Z21749
A/Reference number: Z21749
A/Rocssion: T37852
A/Molecule type: DNA
A/Residues: 178-722 <MUR>
A/Ross-references: EMBL:Z99162; PIDN:CAB16231.1; GSPDB:GN00066; SPDB:SPAC17G6.20c
C/Genetics:
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 *i2 protein - fission yeast (Schizosaccharomyces pombe)
$\text{$Pspecies: Schizosaccharomyces pombe} \text{$Pspecies: Schizosaccharomyces pombe} \text{$Pspecies: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004} \text{$Pspecies: T46560; T37852} \text{$Pspecies: T46560; T47852} \text{$Pspecies: T46560; T47852} \text{$Pspecies: T47852} \text{$Pspeci
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 DB 2; Length 627;
 Score 38; DB 2; Length 723;
Pred. No. 2e+02;
3; Mismatches 3; Indels
 Length 722
 4; Indels
 5; Indels
 Score 38; DB 2; I Pred. No. 1.8e+02;
 DB 2;
 Query Match 50.0%; Score 38; DB 2; Best Local Similarity 50.0%; Pred. No. 2e+02; Matches 8; Conservative 3; Mismatches
 50.0%; Scc. No. 1...
60.0%; Pred. No. 1...
2; Mismatches
 R;Schmidt, H. submidt, H. submitted to the EMBL Data Library, November 1995 **Neference number: Z23067 **A;Reference number: T46560
 265 KKPRKVFDAVVIPVTI 280
 :|||| ||| : ||
133 EKKRKEEAAVAMGVL 147
 1 KKKRKAAAAVLLPVLL 16
 50.0%;
 1 KKKRKAAAAVLLPVL 15
 ||||| : |::|
138 KKXRKKSKKVIMP 150
 Query Match
Best Local Similarity 60.0
Matches 9; Conservative
 1 KKKRKAAAAVLLP 13
 Query Match
Best Local Similarity 53.8
Matches 7; Conservative
A; Note: T12H17.60
 A;Map position: 1
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A;Accession: D84231
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 <STO>
A;Cross-references: UNIPROT:Q9HRE2; GB:AE004437; NID:g10580318; PIDN:AAG19216.1; GSPDB: A;Genetics:
 1 KKKRKAAAAVLLPVL 15
 ||::| || |:|
65 KKEKKRRAAWLSPIL 79
 4 RKAAAAVLLPVLL 16
 14 RKQAAVAILPFLL 26
 8; Conservative
 Query Match
Best Local Similarity
Matches 8; Conserv
 C,Genetics:
A,Gene: yvtA
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 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ms
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accession: AI1291
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1368 GLA>
A;Cross-references: UMIPROT:Q8Y6F0; GB:NC_003210; PIDN:CAC99815.1; PID:g16411191; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmol/37
C;Superfamily: Glycerol dehydrogenase; lactaldehyde reductase homology
 hypothetical protein Vng0737h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C;Accession: D84231
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennia, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NNC-1.
 Glycerol dehydrogenase homolog lin1848 [imported] - Listeria innocua (strain Clip11262)
G.Species: Listeria innocua
G.Species: Listeria innocua
G.Species: Listeria innocua
G.Species: Listeria innocua
G.Species: O. Manocua
G.Species: Listeria innocua
G.Species: Listeria innocua
G.Species: Listeria incoma
G.Species: Li
 A,Cross-references: UNIPROT:Q92AS1; GB:AL592022; PIDN:CAC97079.1; PID:g16414350; GSPDB:GA,Experimental source: strain Clip11262
A; Experimental source: strain Clip11262
A; Genetics:
C; Genetics:
C; Superfamily: Glycerol dehydrogenase; lactaldehyde reductase homology
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 Query Match
49.3%; Score 37.5; DB 2; Length 368;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 2; Mismatches 0; Indels
 'Match 49.3%; Score 37.5; DB 2; Length 368; Local Similarity 76.9%; Pred. No. 1.3e+02; les 10; Conservative 2; Mismatches 0; Indels
 103 KAAAAVLRLPVII 115
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KAAAAVLRLPVII 115
 5 KAAAAVL-LPVLL 16
 KAAAAVL-LPVLL 16
 Query Match
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Cypecies: Bacillus subtiles
Cypereliary Vice Bacillus subtiles
Cypereliary Vice Bacillus subtiles
Cypereliary Vice Bacillus subtiles
Cyperesion: Bacillus Si Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chanter, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
Anathors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell-Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadoie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshikaw, H.; Parro, V.; Yoshikaw, H.; Parro, V.; Yoshikaw, H.; Parro, V.; Yoshikaw, H.; A; Accession: E70048
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: Assach M.; Mulculeic acid sequence not shown; translation not shown
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Residues: 1-121 «KUN»
A;Cross-references: GB:299120; GB:AL009126; NID:g2635613; PIDN:CAB15290.1; PID:e1184379,
A;Experimental source: strain 168
 hypotherical protein CC1709 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87461
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo, M. J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A8461
A;Status: preliminary
A;Molecule type: DNA
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 Score 37; DB 2; Length 121;
Pred. No. 56;
3; Mismatches 4; Indels
Length 74;
 4; Indels
 C, Superfamily: Bacillus subtilis hypothetical protein yvtA
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Score 37; DB
Pred. No. 36;
 1; Mismatches
 hypothetical protein yvtA - Bacillus subtilis
48.7%;
 Query Match 48.7%;
Best Local Similarity 53.3%;
Matches 8; Conservative
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A; Molecule type: DNA
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 Gene: pssA
 A,Cross-ref(
C,Genetics:
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 Gignal peptidase I sipu - Bacillus subtilis
Cibbecies: Bacillus subtilis
Riccession: 19980; 4457077.
Riccession: 19980; 4457077.
Riccession: 19980; 441, 257-259, 1995
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Riccession: 19980; 441, 257-259, 1995
Airthe: Systematic Sequencing of the Bacillus subtilis genome: progress report of the JA; Title: Systematic Sequencing of the Bacillus subtilis genome: progress report of the JA; Airthe: Systematic Sequencing of the Bacillus subtilis genome: progress report of the JA; Airthe: Systematic Sequencing of the Bacillus subtilis genome: progress report of the JA; Airthe: Systematic Sequencing of the Bacillus subtilis genome: progress report of the JA; Airthe: Residues: 17887, Mulls JA; Airthe: Airthe
 CDPGiacylglycerol-serine O-phosphatidyltransferase (EC 2.7.8.8) [similarity] - Mycobacte C; Species: Mycobacterium tuberculosis C; Species: Mycobacterium tuberculosis C; Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C; Accession: B70632 Rscole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
 Cross-references: UNIPROT:0947L3; GB:AE005673; NID:g13423123; PIDN:AAK23685.1; GSPDB:q
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 ch 48.7%; Score 37; DB 2; Length 131;
1 Similarity 68.8%; Pred. No. 60;
11; Conservative 1; Mismatches 2; Indels
 DB 2; Length 187, 84;
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 2 RRAALAVLLIVPVLAA 17
 4 RKAAAAVLL--PVLLA 17
 1 KKKRKAAAAVLLPVLL 16
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KKKRKIKTIVVLSIIM 24
 Query Match
Best Local Similarity
Matches 7; Conserv
 Best Local Similarity
Matches 11; Conserv
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 C;Genetics:
A;Gene: CC1709
 Query Match
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C;Keywords: transferase
F;38-193/Domain: Bacillus subtilis CDPdiacylglycerol-serine O-phosphatidyltransferase ho
 Cispecies: Escherichia coli
Cobate: 31.Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
CiAccession: A30282
R;Choi, Y.L.; Kawase, S.; Nishida, T.; Sakai, H.; Komano, T.; Kawamukai, M.; Utsumi, R.;
Niclaic Acids Res. 16, 7732, 1988
A;Title: Nucleotide sequence of the glpR gene encoding the repressor for the glycerol-3-A;Reference number: A33685; MUID:88319970; PMID:3045764
 A;Molecule type: DNA
A;Residues: 1-299 «CHO»
A;Cross-references: UNIPROT:Q47236; EMBL:X07520; NID:g41582; PIDN:CAA30399.1; PID:g41585
C;Genetics:
 hypothetical protein AGR L 1955 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C; Accession: B98253 R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
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;Cross-references: UNIPROT:Q8U961; GB:AE007870; PIDN:AAK89551.1; PID:g15159433; GSPDB:C
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Natures squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Hitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; WUID:98295987; PMID:9634230
 A;Residues: 1-286 <COL>
A;Cross-references: UNIPROT: P96282; GB:Z84724; GB:AL123456; NID:g3261708; PIDN:CAB06576
A;Experimental source: strain H37Rv
C;Genetics:
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 A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur
A,Reference number: A97359; MUID:21608551; PMID:11743194
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 A;Accession: B70632
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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 Length 299;
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C;Keywords: DNA binding; repressor; transcription regulation
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C;Species: Escherichia coli
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_C
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Pred. No. 1.3e+02;
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Best Local Similarity 50.0%;

Matches 7; Conservative 3
 48.7%;
 ERRKRGGAALLPVI 245
 2 KKRKAAAAVLLPVL 15
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 211 AAAAVĽAPYĽĽ 221
 6 AAAAVLLPVLL 16
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A;Status: preliminary
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outer membrane protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
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A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: F71331
B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.; Altre: Genomic sequence comparison of two unrelated isolates of the human gastric pati
 A;Residues: 1-528 <ARN>
A;Cross-references: UNIPROT:Q9ZLY7; GB:AE001478; GB:AE001439; NID:g4154971; PIDN:AAD0601
A;Cross-references: UNIPROT:Q9ZLY7; GB:AE001478; GB:AE001439; NID:g4154971; PIDN:AAD0601
A;Experimental source: strain J99
C;Genetics:
A;Genetics:
A;Genetics:
C;Guperfamily: Helicobacter pylori hypothetical protein HP0209
 probable membrane protein - Streptomyces coelicolor
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C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36323
R;Oliver: K.; Harris, Date Library, May 1999
A;Reference number: Z21575
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A;Eneriantal source: strain A3(2)
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Caccession: D64603
C;Caccession: D64603
C;Caccession: D6.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn: Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Accession: D64603
A;Access
 C;Superfamily: Streptomyces coelicolor probable integral membrane protein SC3C8.03c
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 2 KKRKAAAAVL----LPVL 15
 4 KKRKVAATLLKRLTLPLL 21
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88 RRKRRAWRAAALLPL 103
 1 KKKRKA--AAAVLLPV 14
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 A; Accession: F71931
A; Status: preliminary
A; Molecule type: DNA
 Query Match
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 hypothetical protein TP0976 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Chacessabon: F71257
R;Fraser, C,M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71257
A;Accession: F71257
A;Accession: F71257
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-459 <COLX
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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Species: Objace: 31.Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: E81723
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUD:20150255; PMID:10684935
A;Accession: E81723
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A,Experimental source: strain Nichols
C;Genetics:
A,Gene: TP0976
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Pred. No. 1.9e+02;
3; Mismatches 4; Indels
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48.7%; Score 37; DB 2; Length 508;
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 1 KKKRKAAA-----AVLLPVLL 16
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| KSKRRFLADTSGNFGMMTAILLPVLL 33
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 A,Gene: AGR_L_1955
A;Map position: linear chromosome
 1 KKKRKAAAAVLLPVL 15
 45 ROSRKISAIPLLPVL 59
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239 QKRKARAITVVPVI 252
 2 KKRKAAAAVLLPVL 15
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A,Status: preliminary
Modecule type: DNA
A,Residues: 1-133 <5TO>
A,Cross-references: UNIPROT:Q9SJT2, GB:AE002093; NID:g4567277; PIDN:AAD23690.1; GSPDB:G?
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C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Accession: F84486

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Filn, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Suiz, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, u. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: F84486

A;Accession: Psalannary

A;Accuse and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Accession: Psalannary

A;Accuse and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Accession: Psalannary

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A;Accession: Carron Carr
 probable retroelement pol polyprotein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (1.5pecies: Arabidopsis thaliana (mouse-ear cress) (1.5pecies: Arabidopsis thaliana (mouse-ear cress) (1.5pecies: O2-feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 (1.5pecies: O3-feb) (1.
 Score 37; DB 2; Length 135
Pred. No. 5.3e+02;
5; Mismatches 2; Indels
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 A;Map position: 2
C;Superfamily: retrovirus-related polyprotein
 C; Superfamily: retrovirus-related polyprotein
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Conservative
 48.7%;
 1 KKKRKAAAAVLLPV 14
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69 EKRRKARSAIVLSV 82
 1 KKKRKAAAAVLLPV 14
 :||:|| :|::| |
EKKKKARSAIVLSV 82
 Best_Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity
 Search completed: June
Job time : 19.2812 secs
 A; Accession: E84601
 A, Gene: At2g07550
A, Map position: 2
 A; Gene: At2g21460
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 Cross-references: UNIPROT:025379; GB:AE000580; GB:AE000511; NID:92313792; PIDN:AAD0773
 denvlate cyclase (BC 4.6.1.1) - Trypanosoma cruzi
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A;Axiol.coulte type: DNA
A;Residues: 1-1248
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F;248-253/Region: nucleotide-binding motif B
F;252-255/Region: DEAH motif
 | | | | | ||:|:|
420 KNAIKKAVADLLPILVA 436
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535 KAKRKKRGYIILPIAL 550
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 1 KKKRKAAAAVLLPVLLA
 3 KRKAAAAVLLPVLL 16
A;Residues: 1-607 <TOM>
 A;Start codon: GTG
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OM protein - p. Run on:	Title: Perfect score, Sequence: Scoring table: Searched:	Total number of Minimum DB seq Maximum DB seq Post-processing	Database :	Pred. No score great and is digital from the score No. Score	

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Adp29329 Human sec Aar86406 Human mat Aar86407 Human mat Aar75648 Human pla Aaw52134 Rabbit me Aab86416 Amino aci Aae104234 Human mat Aae21037 Human mem Aam50865 Matrix me Aam50865 Matrix me Adc15498 Human bas	Add64179 Human Pro Ad664177 Rat Prote Adf13708 Tumor-Ass Adf13708 Tumor-Ass Adf13708 Tumor-Ass Adf13708 Tumor-Ass Adf13703 Human mat Abm81541 Tumour-as Adg23426 PRO Polyp Ab57896 Drosophil Aae12503 Wembrane Aae12478 Wembrane Aae12478 Wembrane Aae12478 Wembrane Aae12478 Wembrane Aae12478 Staphyloc Ab672202 Staphyloc Abm72922 Staphyloc Ab6707202 Staphyloc Ab6707202 Staphyloc Ab88790 Membrane Aau00647 Human mem Ad0688790 Membrane Ab975441 Wembrane Ab97543 Membrane Ab97543 Membrane Ab97543 Membrane Ab97543 Membrane Ab97543 Membrane Ab97543 Membrane Ab97543 Membrane Ab97543 Membrane Ab97543 Membrane Ab97543 Membrane	Abg758434 Membrane Abg758434 Membrane Abb09891 Amino aci Abb09891 Amino aci Abb09891 Amino aci Abb09891 Amino aci Abb039897 Propionib Aam03984 Human imm Abp41851 Human imm Abp41851 Human imm Abb6722 Drosophil Abo69672 E. faeciu Abo69672 Breudomon Abb6738 Pseudomon Abb6722 Drosophil Abo7538 Pseudomon Abb6722 Drosophil Abb6722 Drosophil Abb6722 Drosophil Abr52831 Protein s Adv62261 Disease t Abb14908 Mutant pe Abp8758 Antimicro Abp89758 Antimicro Abp89758 Antimicro Abp98758 Self-asse Abp59422 Self-asse Abp59423 Self-asse Abp59423 Self-asse
41 53.9 549 8 41 53.9 579 2 41 53.9 582 2 41 53.9 582 2 41 53.9 582 4 41 53.9 582 4 41 53.9 582 4 41 53.9 582 5 41 53.9 582 5	183 41 53.9 582 7 ADECA179 184 41 53.9 582 7 ADECA179 186 41 53.9 582 7 ADECA179 186 41 53.9 582 7 ADECA179 188 41 53.9 582 7 ADECA179 188 41 53.9 582 8 ADECA179 189 41 53.9 582 8 ADECA164 190 40.5 53.3 288 4 ADECA164 191 40.5 53.3 288 4 ADECA164 192 40 52.6 20 4 AACR4948 193 40 52.6 20 4 AACR2930 194 40 52.6 20 4 AACR2930 195 40 52.6 238 7 ABC71291 196 40 52.6 238 7 ABC71291 197 40 52.6 534 6 ABC7266 198 40 52.6 534 6 ABC7266 199 40 52.6 534 6 ABC7266 199 40 52.6 534 6 ABC7266 201 40 52.6 534 6 ABC7266 202 40 52.6 534 6 ABC7266 203 51.3 9 7 ADECA179 204 39 51.3 9 7 ADECA179 205 39 51.3 9 7 ADECA179 206 39 51.3 11 7 ADECA179 211 39 51.3 11 7 ADECA179 212 39 51.3 11 7 ADECA179 213 39 51.3 11 7 ADECA179 214 39 51.3 11 8 ABC75432 215 216 39 51.3 11 8 ABC75432 216 39 51.3 11 8 ABC75432 217 39 51.3 11 8 ABC75432 218 39 51.3 11 8 ABC75432	39 51.3 13 8 8 51.3 13 8 8 51.3 13 8 8 51.3 13 8 8 51.3 13 8 8 51.3 13 8 8 51.3 13 8 8 51.3 13 8 8 51.3 13 8 8 51.3 13 8 8 51.3 10 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
Adq91936 Kaposi fi Adq80671 Kaposi FG Adx1973 Heat shoc Adx1762 Membrane Abg68407 Membrane Abg68407 Membrane Adb88779 Membrane Adb877430 Membrane Adv8075479 Membrane Adv8075476 Membrane Adv87754778 Membrane	Add 17601 Membrane Add 17601 Membrane Add 17601 Membrane Add 17819 Coll pene Abg 7919 Coll pene Add 7919 Human C35 Add 5087 Human C35 Add 5081 Human C35 Add 5082 Human C35	Human C3 Human C4 Human C4 Human C4 Human C4 Human C5 Human C6 Human C7 Hum
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6 ABU82089 6 ABJ72369 6 ABJ72397 6 ABJ72397 7 AbB772397 7 ADB80680 7 ADB80680 7 ADB80680 7 ADB84951 7 ADB84951 7 ADB84951 7 ADB84951 7 ADB84951 7 ADB84951 7 ADC36813 7 ADC36813 7 ADC36813 7 ADC36813 7 ADC49033 7 ADC49033 7 ADC49031 7 ADD10655 7 ADD10655 7 ADD10655 7 ADD50475 7 ADD50475 7 ADD50475 7 ADD50475 8 ADD50475 8 ADD50475 8 ADD50475 8 ADD50475 8 ADD50475 8 ADD50435 8 ADD850435 8 ADD850435 8 ADD850435 8 ADD850435 8 ADD850435 8 ADD850435 8 ADD850435 8 ADD850435 8 ADD850435 8 ADD8504381 8 ADD8504381	8 ADD77319 8 ADD77531 8 ADD74047 8 ADD74047 8 ADD74023 8 ADD76023 8 ADD76023 8 ADD76821 8 ADD76821 8 ADD76821 8 ADD76821 8 ADD76821 8 ADD77667 8 ADD77667 8 ADD77667 8 ADD77667 8 ADD7767 8 ADD73801 8 ADD73810
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Aae22157 Human TRN Adp41137 Human sec Adp41137 Human sec Ada00875 Mouse ESD Ada00875 Mouse ESD Ada00873 Human DSD Ada00873 Human DSD Adf61256 Human Dro Abm25701 Human dia Adf77181 KALPA, 2/ Adg70297 Novel hum Ade608079 Novel hum Ade608079 C. neofor Adw70293 C. neofor Adw70293 C. neofor Adw55543 Toxin Tca Abb58602 Drosophil Aww56543 Toxin Tca Abb58602 C. neofor Adw56393 C. neofor Adw6680 Human nov Add12701 Human nov Add12701 Human nov Add12701 Human nov Add12701 Human col Adw6680 Klebsiell Adg7100 Human col Adw6680 Klebsiell Adg7100 Human col Adw6680 N. gonorr Adw6680 N. gonorr Adw6680 N. gonorr Adw6880 Protein e Adw62216 Transcrip Adl3319 Human ser Adw62216 Transcrip Adl3202 Human ser Adw4679 Propionib Adm4198 Propionib Adm4198 Propionib Adm4198 Propionib	
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Adg11893 Novel Adf94550 Novel Adg06646 Human Adh3890 Novel Adh43799 Human Adg34080 Novel	Humar Humar NOV3	Nove] Nove] Himay	Humar Humar	Humar Marke		Abu79148 Chemok	Adf43317 Superanti	Adn74359 Thale	Ad844821 Bacterial Abg07433 Novel hum	Ads32637 Sequence	Abu70702 Human adi	~ ~	Abm84893 Human	Abm84892 Human	Abu40835 Protein e Adf04701 Bacterial	Abo78467 Pseudo	Abm84891 Human dia	Ads28516 Bacter Ade08682 Novel	Adn99232 Novel	Human	Adb80480 Ovaria Ade62796 Human	Ade61993 Human Pro	Ade56238 Human	Ade61997 Human Adi78509 Human	Adm43151 Human	Ad182833 Human Ado05712 Human	Abb60230 Drosor	Ads41573 Bacter	Abu33993 Protei	Abo69542 Pseudo	Human	Abu43960 Protei	Abb54167 Lactococc	Abb59870 Drosophil	Σΰ	runga. Human	Human	Human	Aab19590 Human C Adn39875 Cancer/
£0000000000000000000000000000000000000	50 44 09	05 02 44	60 88	08 31	00	8 6 6	200	r 0. 1	21 33	37 68	02	11 61	93	95	35 01	67	91	16 82	32	833	080	93	38	97	511	33 12	30	73	93	42	97	09	67	70		94.	18 77	9.4	90 75
B ADG11993 8 ADF94550 8 ADG06646 8 ADH38990 8 ADH43799																																							
4444444 000000																																							
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The sequence represents a human membrane translocated peptide (WTLP).

WTLPs and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer lining the gastrointestinal tract), cith the directly or from a pharmaceutically active agent loaded particle, into the dirculatory spatem of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the identification of WTLPs which retain the functional activity of a fullength WTLP, as a cell-based screen for assaying the functional activity of a MTLP and characterising the properties of a MTLP, for diagnosis of a pathological disorder (by administration of a WTLP-active agent complex or mTLP-active particle complex comprising a diagnostic agent) and for preventing or treating a pathological disorder
 Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic
 Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
 100.0%; Score 76; DB 4; Length 17; 100.0%; Pred. No. 1.3e-05; ive 0; Mismatches 0; Indels
 Human membrane translocating peptide (MTLP) #23
 AAU00654 standard; peptide; 17 AA
 100.0%; Fr.
 Claim 2; Page 11; 42pp; English
 ADB88797 standard; peptide; 17
 1 KKKRKAAAAVLLPVLLA 17
 1 KKKRKAAAAVLLPVLLA 17
 99US-0156246P
 27-SEP-2000; 2000WO-IB001491
 07-SEP-2001 (first entry)
 O'mahony DJ, Lambkin IJ;
 Local Similarity 100.
nes 17; Conservative
 (OMAH/) O'MAHONY D J. (LAMB/) LAMBKIN I J.
 WPI; 2001-300212/31.
N-PSDB; AAS00648.
 the peptides.
 Sequence 17 AA;
 WO200127154-A2.
 27-SEP-1999;
 Homo sapiens.
 19-APR-2001.
 AAU00654;
 Query Match
 Matches
 RESULT 2
ADB88797
ID ADB8
XX
AC ADB8
XX
DT 04-D
XX
DE Memb
 AMU0654
AAU00654
AAU00664
AAU0
 Antagonis
Human ova
Human sec
C glutami
Amino aci
Novel hum
Novel hum
 Polypepti
Human hos
Novel hum
Novel hum
 Human car
Arabidops
Arabidops
Arabidops
Tumour-as
Arabidops
Arabidops
Arabidops
Arabidops
Human ORF
 Human pol
Arabidops
Arabidops
 Propionib
Propionib
Neisseria
 Arabidops
Arabidops
Arabidops
Arabidops
Thermococ
 Kinase 45
G-coupled
Human G-c
Human ova
 Protein e
Drosophil
 Hydrophob
Human sof
 Staphyloc
Staphyloc
 ORF
 Protein e
 Human hos
 Bacterial
 N. gonorz
 Human Novel
 Human
Novel
Human
 Mouse
 Human
 Human
 Human
 Human
 Human
 Add 46123
Add 90451
Add 90551
ADE46123
ADJ07541
AAG43291
AAG43291
AAG43291
AAG2489
AAG2483
AAG43296
AAG483
AAG483
AAG483
AAG483
AAG483
AAG483
AAG483
AAG483
AAG4834
AAG54932
AAG64932
AAG64932
AAG64932
AAG64932
AAG64932
 AAG39044
AAG28085
AAG39043
AAG39043
ADN47148
AAG39042
ABB89527
ABB89527
ABB89527
ABB89527
ABB89527
ABB89527
ABB89527
 AAU37492
AAU34410
AAB85724
ABU39633
ABB70799
 AAB41505
ABG10620
 ADK40924
 \begin{array}{c} 1 & 11 & 11 & 11 & 11 & 11 \\ 1 & 11 & 11 & 11 & 11 \\ 1 & 11 & 11 & 11 \\ 1 & 11 & 11 &
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ALIGNMENTS

Membrane translocating peptide #23

04-DEC-2003 (first entry)

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Gaps

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The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mana. Is a nucleic acid coding for a protein, the level of which or its mana. Is greater than in a non-Peyer's patch cell. The preferred protein of the invention is a transcription factor or a protein that activates a transcription factor selected from Jun-B, c-jun related TF, Jun-D, STAT 3 companal transducer and activator of transcription 3, NKappasbapri Tf plos subunit, S-myc proto-oncogene, myc related, NM2-M2, nucleoside diphosphate kinase B, metastasis reducing protein, and C-est-I protocomocogene, and psy. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein CD5 precursor, HSP concepted from the group. The method is useful for increasing or protein selected from the group. The method is useful for increasing or decreasing antigen or vaccine delivery to M cells. The method may also be used to enhance transport of a drug through the gastrointestinal tract function is a membrane translocating peptide of the
 ö
 Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
 Gaps
 Peyer's patch cell; non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell; membrane translocating peptide.
 ;
0
 100.0%; Score 76; DB 7; Length 17; 100.0%; Pred. No. 1.3e-05;
 Indels
 Membrane translocating peptide; transmembrane transport; enzymatic degradation; gastrointestinal tract.
 Mismatches
 Example 6; Page 51; 147pp; English.
 Membrane translocating peptide #23.
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 Brayden
 ;
0
 ABG75448 standard; peptide; 17
 17
 1 KKKRKAAAAVLLPVLLA 17
 04-APR-2002; 2002WO-IB003866.
 04-APR-2001; 2001US-0281387P
 02-JUL-2001; 2001US-0302591P
 KKKRKAAAAVLLPVLLA
 (first entry)
 Local Similarity 100.
1es 17; Conservative
 O'mahony DJ, Byrne D,
 (OMAH/) O'MAHONY D J.
 WPI; 2003-229409/22
 WO2003004646-A2
 Sequence 17 AA;
 Unidentified
 Unidentified
 15-APR-2004
 16-JAN-2003
 ABG75448;
 Query Match
 Best Loc
Matches
 RESULT 3
 ABG75448
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The present invention relates to a composition which comprises a translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment of at least 4 amino acids of the transport peptide. The composition is useful in treating a pathological disorder in an animal, as it protects an orally delivered active agent from enzymatic degradation in the gastrointestinal tract (GIT), and promotes absorption across epithelial cells lining the GIT. The present sequence is a polypeptide used in the exemplification of the invention
 comprises a translocating peptide, consisting of a transport peptide, an
extended peptide comprising the transport peptide or a transport-active
 Cellular protein; nuclear translocation; nuclear localization signal; immunosuppressant; immune response; viral infection; immune disorder; rheumatoid arthritis; multiple sclerosis; juvenile-onset diabetes; NLS; systemic lupus erytematosus; SLE; asthma; sepsis; tumor growth; SV40; fibroblast growth factor; SV40 large T antigen.
 Composition, useful for treating a pathological disease in an animal,
 Gaps
 ö
 Length 17;
 Indels
 /note= "modified by epsilon-dansyl"
 Pinilla C;
 100.0%; Score 76; DB 8; L
100.0%; Pred. No. 1.3e-05;
ive 0; Mismatches 0;
 /note= "C-terminal amide"
 Houghten R,
 Location/Qualifiers
 AAY55835 standard; peptide; 29 AA.
 Claim 1; Page 25; Opp; English.
 1 KKKRKAAAAVLLPVLLA 17
 21-APR-2003; 2003WO-US012543
 SV40MEM polypeptide fragment.
 99WO-US008984.
 19-APR-2002; 2002US-00126845
 KKKRKAAAAVLLPVLLA
 06-MAR-2000 (first entry)
 Lambkin I,
 Local Similarity 100.
108 17; Conservative
 WPI; 2004-034528/03.
 (SARL-) SARLAN LTD
 40.
 WO2003089458-A2
 Sequence 17 AA;
 Key
modified_site
 modified_site
 В,
 Synthetic.
Simian virus
 26-APR-1999;
 WO9957138-A1
 30-0CT-2003
 11-NOV-1999
 AAY55835;
 fragment.
 O'mahony
 Query Match
 Best Loc
Matches
 RESULT 4
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31-OCT-2002,
 RESULT 6
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 KW inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma; hammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma; hammatory disorder; hyper-IgM syndrome; viral infection; asthma; hypehidrotic ectodermal dysplasia; al incontinentia pigmenti; kW x-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti; kW x-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti; kW influenza; rheumatorid arthritis; inflammatory bowel disease; colitis; atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAB; kM axperimental allergic encephalomyelitis; autoimmune disorder; wound; kW birth defect; necrotic lesion; organ transplant rejection; pancreas; kW signal transduction; hyperoliferative disorder; huntington's chorea; kW vitamin B12 malabsorption; neurological disorder; Huntington's chorea; kW infertility; psoriasis; haemolytic anaemia; antiinflammatory; anti-HIV; kW cytostatic; hepatortoropic, vitrode; antitallergic; antiallergic; antiallergic; antitallergic; antitalle
 The invention provides a composition comprising an isolated polypeptide (I) (polypeptide inhibitor of a cellular protein nuclear translocation) which comprises a signal sequence peptide capable of delivering (I) through a cytoplasmic membrane into the cell; and a nuclear localization signal sequence (NLS) present along with an immunosuppressant. (I) or its derivatives provide useful tools for introducing an exogenous polypeptide comprising an NLS into an intact cell to inhibit nuclear translocation of a cellular protein, for studying the role of nuclear translocation in the regulation of cellular processes. See AAYSS812 for detailed uses of (I) and compositions containing (I). The present sequence represents a polypeptide fragment comprising the hydrophobic region of the signal peptide from fibroblast growth factor and the SV40 large T antigen NLS
 Novel composition comprising a nuclear localization signal and an inhibitor of nuclear translocation, useful for preventing transplanted
 1; Gaps
 Human; nuclear factor-kappaB; NF-kappaB; immune disorder; cancer;
 Query Match 70.4%; Score 53.5; DB 3; Length 29; Best Local Similarity 77.8%; Pred. No. 0.12; Matches 14; Conservative 0; Mismatches 3; Indels
 Human NF-kappaB inhibitory peptide.
 ABU69594 standard; peptide; 29 AA.
 Claim 11; Page 42; 68pp; English.
 (BRIM) BRISTOL-MYERS SQUIBB CO.
 |||||| || ||| ||||| KKKRKVAAVALLPAVLLA 19
 1 KKKRKAAAAVLLP-VLLA 17
 98US-00072429
 05-JUN-2003 (first entry)
 organ or tissue rejection.
 antiarteriosclerotic.
 WPI; 2000-062141/05.
 Sequence 29 AA;
 04-MAY-1998;
 ABU69594;
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WO200286076-A2

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The present invention relates to the isolation of human nuclear factor-kappaB (NP-kappaB) associated polypetides and polynucleotides. The NF-kappaB (NP-kappaB) associated polypetide and polynucleotide sequences are useful for preventing, treating or ameliorating various disorders including immune disorders, inflammatory disorders, cancers, disorders relating to disorders, inflammatory disorders, cancers, disorders relating to disorders, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, x-linked anhidrotic ectodermal dysplasia, immunodeficiency, all concentinentia pigmenti, viral infections (e.g. those caused by human immunodeficiency virus (HIV), human T-cell lymphotropic virus (HIV), hepatitis B, hepatitis G, pstein Barr virus (BBN), influenza), crheumatorid arthritis, inflammatory bowel disease, collits, asthma, atherosclerosis, cachexia, enthyroid sick syndrome, stroke, experimental allergic encephalomyelitis (BAE), autoimmune disorders, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, disorders related to aberrant signal transplant rejection, disorders related to aberrant signal cransduction, hyperproliferative disorders, syndrome, bacterial disorders (e.g. diabetes mellitus, vitamin B12 malabsorption), neurological conficents, cardiovascular disorders, infertility, psoriasis and haemolytic anaemia. The present sequence represents a human NF-kappaB inhibitory peptide used to identify the NF-kappaB associated the hovention control organic control organic control organic careacters.
 ä
 SV40MEM polypeptide; signal peptide; fibroblast growth factor; SV40 large antigen; nuclear localisation signal; NLS; INLS; Inhibition; nuclear translocation inhibitor; kappa immunoglobulin light chain expression; S. typhosa LPS; nuclear translocation; treatment; immune disorder; autoimmune disease; hypereenstitivity; sepsis; prevention; septic shock; antiviral agent; tumour growth suppressor.
 Novel NF-kappaB-associated polypeptides and polynucleotides useful for diagnosing, treating and preventing cancer, hepatic disorders, aberrant apoptosis, viral infections, autoimmune disorders, asthma and stroke.
 Gaps
 SV40MEM polypeptide used to inhibit kappa-Ig light chain expression.
 ï
 Score 53.5; DB 6; Length 29;
Pred. No. 0.12;
 3; Indels
 0; Mismatches
 AAW56391 standard; peptide; 30 AA.
 Disclosure; Fig 1; 608pp; English.
 (BRIM) BRISTOL-MYERS SQUIBB CO
 2 KKKRKVAAVALLPAVLLA 19
 1 KKKRKAAAAVLLP-VLLA 17
 Carman J, Feder J, Nadler S;
 19-APR-2001; 2001US-0284962P.
26-APR-2001; 2001US-0286645P.
09-JAN-2002; 2002US-0346986P.
19-APR-2002; 2002WO-US012636.
 70.4%;
 05-AUG-1998 (first entry)
 Query Match
Best Local Similarity 77.8
Matches 14; Conservative
 Sequence 29 AA;
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Synthetic. Simian virus 40.

W09957138-A1

11-NOV-1999

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RESULT
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 The present sequence represents the SV40MEM polypeptide, which comprises the hydrophobic region of the signal peptide from fibroblast growth active and the SV40 large antigen nuclear localsation signal (NLS). The gator and the SV40 large antigen nuclear localsation signal (NLS). The peptide has immunosuppressive activity, and causes an approximately 75-SV40 inhibition of kappa immunoglobulin (19) light chain expression in cresponse to S. typhosa LPS. L. and D-forms of the SV40MEM peptide are equally effective. The SV40MEM polypeptide exemplifies the nuclear translocation inhibitor polypeptide of the invention. Nuclear CC translocation inhibitor polypeptide comprise a signal sequence peptide capable of delivering the polypeptide through the cytoplasmic membrane into a cell, and at least 2 nuclear localisation sequences (NLSS). The COLYPEPTIGE capable of delivering the polypeptide through the cytoplasmic membrane copyplicates can be used to inhibit nuclear translocation of certain cellular protein. In-addition, since the nuclear translocation of certain cellular computed inhibitors are useful as immunosuppression agents. The colypeptides can therefore be usef for the treatment of immune disorders including autoimmune diseases. The polypeptides can also be used for the treatment of sepsis and in thiste a state of hypersensitivity, for the treatment of sepsis and in the prevention of septic shock, antiviral agents, tumour growth
 ï
 Nuclear translocation inhibitor polypeptides - comprising signal sequence for delivery through the cytoplasmic membrane and at least 2 nuclear localisation sequences.
 Cellular protein, nuclear translocation; nuclear localization signal; immunosuppressant; immune response; viral infection; immune disorder; rheumatodia arthritis; multiple sclerosis; juvenile-onset diabetes; NLS; systemic lupus erytematosus; SLE; asthma; sepsis; tumor growth; SV40; fibroblast growth factor; SV40 large T antigen.
 Gaps
 ٠<u>.</u>
 70.4%; Score 53.5; DB 2; Length 30; 77.8%; Pred. No. 0.12; 1ve 0; Mismatches 3; Indels
 Cleaveland JS, Blake J, Haffar OK;
 AAY55812 standard; peptide; 30 AA.
 Claim 15; Page 28; 69pp; English
 (BRIM) BRISTOL-MYERS SQUIBB CO.
 KKKRKVAAVALLPAVLLA 19
 1 KKKRKAAAAVLLP-VLLA 17
 97US-00928958.
 97WO-US016217.
 96US-0026978P
 SV40MEM polypeptide fragment.
 (first entry)
 Local Similarity 77.8 les 14; Conservative
 WPI; 1998-217028/19.
 Sequence 30 AA;
 cellular genes
 WO9811907-A1.
 15-SEP-1997;
 20-SEP-1996;
12-SEP-1997;
 06-MAR-2000
 Nadler SG,
 26-MAR-1998
 Synthetic.
 AAY55812;
 Query Match
 Best Loc
Matches
 RESULT 7
 AAY55812
g
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The invention provides a composition comprising an isolated polypeptide (I) (polypeptide inhibitor of a cellular protein nuclear translocation)

which comprises a signal sequence poptide capable of delivering (I) through a cytoplasmic membrane into the cell; and a nuclear localization signal sequence (NLS) present along with an immunosuppressant. (I) or its derivatives provide useful tools for introducing an exogenous polypeptide comprising an NLS into an intact cell to inhibit nuclear translocation of a cellular protesin, for studying the role of nuclear translocation in the cregulation of cellular processee. (I) along with other immunosuppressants are useful as immunosuppression compositions, used for preventing or tissue in a subject, preferably mammals. Administration of antiviral amounts of the composition into a subject is useful for treating or preventing a viral infection. The composition also is useful in the treatment of a wide variety of immune disorders such as rheumatoid arthritis, multiple sclerosis, juvanile-onset diabetes, systemic lupus crytematosus (SLB), autoimmune uveoretinitis, autoimmune oophoritis, cron's disease, sarcoidosis, rheumatic carditis, antoimmune oophoritis, Cron's disease, sarcoidosis, rheumatic or organs. They are also useful for treating physical symptoms include actime or organs. They are also useful for treating physical symptoms manifested by response to allergens which can initiate a state of hypersensitivity, or which can provoke a hypersensitivity reaction of transplanted tissue or organs. They are also useful for treating physical symptoms include asthma, joint swelling and urticaria. Additionally, due to the superior immunosuppressive treatment of sepsis and in the prevention of septic shock. They are also used as antiviral agents and also can be used to suppress tumor growth. Immune suppression than either treatment alone. The composition contact the composition of treatment alone. The composition contact the composition of the prevention of the prevention of treatm
 immunosuppressant or polypeptide alone. The present sequence represents SV40MEM polypeptide fragment comprising the hydrophobic region of the signal peptide from fibroblast growth factor and the SV40 large T antigen
 suppression than either treatment alone. The composition exhibits
 Novel composition comprising a nuclear localization signal and an inhibitor of nuclear translocation, useful for preventing transplanted
 Gape
 superior immunosuppressive characteristics compared to using an
 ä
 Score 53.5; DB 3; Length 30;
Pred. No. 0.12;
0; Mismatches 3; Indels
 3; Indels
 Example 1; Page 26; 68pp; English.
 (BRIM) BRISTOL-MYERS SQUIBB CO.
 .
 1 KKKRKAAAAVLLP-VLLA 17
 99WO-US008984.
 98US-00072429.
 70.48;
 77.8%;
 organ or tissue rejection.
 Query Match
Best Local Similarity 77.8
Matches 14; Conservative
 WPI; 2000-062141/05.
 Sequence 30 AA;
26-APR-1999;
 04-MAY-1998;
 Nadler SG;
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1;

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2 KKKRKVAAVALLPAVLLA

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us-10-764-235-24.rag

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The specification describes a lipid-nucleic acid complex, comprising a compacted nucleic acid, a polycation, a targeting factor and a lipid, but not a protamine. The targeting factor increases cellular bioavailability of the nucleic acid without interaction with a specific outer cell surface membrane receptor. The mean diameter of the complex is greater than 100 nm and less than 400 nm. The lipid-nucleic acid complex is useful for delivering a nucleic acid to a cell in vivo, e.g. for gene therapy. It reduces levels of inflammatory cytokines such as tumour necrosis factor-alpha. The complex is useful for manufacturing a neciosament for treating or diagnosing a variety of diseases, conditions or syndromes such as cancer, bacterial, viral or parasitic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited translocating peptide, which is used as the targeting factor in lipid-nucleic acid complexes of the invention
 Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
Lipid-nucleic acid complex; polycation; targeting factor; gene therapy; cancer; infection; immune deficiency; gene defect; genetic disease; membrane translocating peptide.
 Peyer's patch cell, non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell; membrane translocating peptide.
 Score 53; DB 6; Length 16;
Pred. No. 0.076;
 1; Indels
 Harvie P, Paul R, Cudmore S, O'mahony DJ;
 1; Mismatches
 Disclosure; Page 10; 259pp; English.
 ADB88776 standard, peptide; 16 AA.
 Membrane translocating peptide #2.
 (TARG-) TARGETED GENETICS CORP. (EMER-) EMERALD GENE SYSTEMS LTD.
 30-APR-2002, 2002WO-US013609.
 30-APR-2001; 2001US-0287786P.
 69.7%;
 4 RKAAAAVLLPVLLA 17
 (first entry)
 Local Similarity 85.7 tes 12; Conservative
 WPI; 2003-183837/18,
 WO2003004646-A2.
 Sequence 16 AA;
 WO200288318-A2.
 Unidentified
 04-DEC-2003
 07-NOV-2002.
 16-JAN-2003
 ADB88776;
 Query Match
 Matches
 RESULT 10
 ADB8877
 BXBX8X444XBXBXBXB
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 ö
 Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic
 The sequence represents a human membrane translocated peptide (WTLP). WTLPs and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer example, an epithelial cell layer lining the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle, into the circulatory system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the dentification of MTLPs which retain the functional activity of a MTLP, as a cell-based screen for assaying the functional activity of a MTLP, and characterising the properties of a MTLP, for diagnosis of a pathological disorder (by administration of a MTLP-active agent complex or MTLP-active particle complex comprising a diagnostic agent) and for preventing or treating a pathological disorder.
 Membrane translocating peptide, MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
 Gaps
 Amino acid sequence of membrane translocating peptide ZElan094.
 ö
 4; Length 16;
 1; Indels
 Human membrane translocating peptide (MTLP) #2.
 Score 53; DB 4;
Pred. No. 0.076;
1; Mismatches
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 AAU00633 standard; peptide; 16 AA.
 Claim 2; Page 11; 42pp; English.
 ABP70215 standard; peptide; 16
 27-SEP-2000; 2000WO-IB001491.
 99US-0156246P
 4 RKAAAAVLLPVLLA 17
:| |||||||||
1 KKKAAAVLLPVLLA 14
 (first entry)
 (first entry)
 O'mahony DJ, Lambkin IJ;
 Local Similarity 85.7 es 12; Conservative
 (OMAH/) O'MAHONY D J. (LAMB/) LAMBKIN I J.
 WPI; 2001-300212/31.
 N-PSDB; AAS00627.
 the peptides.
 Sequence 16 AA;
 WO200127154-A2.
 Homo sapiens.
 27-SEP-1999;
 07-APR-2003
 07-SEP-2001
 19-APR-2001
 Query Match
Best Local Si
Matches 12;
 ABP70215;
 AAU00633;
 RESULT 9
 AAU00633
 ABP7021
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 22225222
22225
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Gaps

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 The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mRNA is greater than in a non-Peyer's patch cell. The preferred protein of the invention is a transcription factor or a protein that activates a transcription factor or a protein that activates of transcription 3, NK appasabyr; T plus cull transducer and activator of transcription 3, NK appasabyr; T plus subunit, S-myc proto-oncogene, myc related, NM3-M2, nucleoside diphosphate kinase B, metastasis reducing protein, and C-est-I protoconcogene, and psy. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein of the invention is concogene, and psy. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein CS precursor, HSP CC 84, and Ca2+ dependent phospholipase A2 precursor and the mRNA is for a protein selected from the group. The method is useful for increasing or decreasing the level of a protein in a Peyer's patch cell, particularly cin increasing antigen or vaccine delivery to M cells. The method may also be used to enhance transport of a drug through the gastrointestinal tract increasing a membrane translocating peptide of the
 ö
 Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
 Gaps
 Lipid-nucleic acid complex; polycation; targeting factor; gene ther cancer; infection; immune deficiency; gene defect; genetic disease;
 Amino acid sequence of membrane translocating peptide ZElan094R.
 ö
 Score 53; DB 7; Length 16;
Pred. No. 0.076;
1; Mismatches 1; Indels
 Example 6; Page 51; 147pp; English,
 ä
 ABP70216 standard; peptide; 20 AA.
 Brayden
 membrane translocating peptide.
 04-APR-2002; 2002WO-IB003866.
 04-APR-2001; 2001US-0281387P. 02-JUL-2001; 2001US-0302591P.
 30-APR-2002; 2002WO-US013609
 30-APR-2001; 2001US-0287786P
 4 RKAAAAVLLPVLLA 17
 (first entry)
 12; Conservative
 'n
 (OMAH/) O'MAHONY D J.
 O'mahony DJ, Byrne
 WPI; 2003-229409/22.
 Sequence 16 AA;
 WO200288318-A2
 Unidentified
 07-APR-2003
 07-NOV-2002
 ABP70216;
 Query Match
Best Local S
 Matches
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The specification describes a lipid-nucleic acid complex, comprising a compacted nucleic acid, a polycation, a targeting factor and a lipid, but not a protamine. The targeting factor increases cellular bioavailability of the nucleic acid without interaction with a specific outer cell surface membrane receptor. The mean diameter of the complex is greater than 100 nm and less than 400 nm. The lipid-nucleic acid complex is useful for delivering a nucleic acid to a cell in vivo, e.g. for gene therapy. It reduces levels of inflammatory cytokines such as tumour cerosis factor-alpha. The complex is useful for manufacturing a medicament for treating or diagnosing a variety of diseases, conditions or syndromes such as cancer, bacterial, viral or paralic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited canabicating peptide, which is used as the targeting factor in lipid-tucleic acid complexes of the invention
 ö
 Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
 Lipid-nucleic acid complex, polycation, targeting factor; gene therapy, cancer; infection; immune deficiency, gene defect; genetic disease.
 /note= "S(galactose), cholesteryl-succinyl, DOPE-
succinyl, DSPE-PEGSK-succinyl, DMPE-PEGSK-succinyl, or
DSPE-PEGSK-succinyl attached"
 Gарв
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0
 Length 20;
 1; Indels
 Amino acid sequence of targeting factor Gelan094.
 Score 53; DB 6;
Pred. No. 0.096;
 O' mahony DJ;
 Harvie P, Paul R, Cudmore S, O'mahony DJ;
 Mismatches
 Disclosure; Page 10; 259pp; English.
 Location/Qualifiers
 ABP70234 standard; peptide; 15 AA.
(TARG-) TARGETED GENETICS CORP.
(EMER-) EMERALD GENE SYSTEMS LTD.
 (TARG-) TARGETED GENETICS CORP.
(EMER-) EMERALD GENE SYSTEMS LTD.
 Cudmore S,
 Match 69.7%;
Local Similarity 85.7%;
les 12; Conservative 1
 30-APR-2002; 2002WO-US013609.
 30-APR-2001; 2001US-0287786P.
 4 RKAAAAVLLPVLLA 17
 1 KKKAAAVLLPVLLA 14
 07-APR-2003 (first entry)
 WPI; 2003-183837/18
 Paul R,
 Sequence 20 AA;
 WO200288318-A2.
 Key
Modified-site
 Unidentified
 07-NOV-2002
 Harvie P,
 ABP70234;
 Matches
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 compacted nucleic acid, a polyation, a targeting factor and a lipid, but not a protamine. The targeting factor increases cellular bloavailability of the nucleic acid without interaction with a specific outer cell surface membrane receptor. The mean diameter of the complex is greater than 100 nm and less than 400 nm. The lipid-nucleic acid complex is useful for delivering a nucleic acid to a cell in vivo, e.g. for gene therapy. It reduces levels of inflammatory cytokines such as tumour necrosis factor-alpha. The complex is useful for manufacturing a medicament for treating or diagnosing a variety of diseases, conditions or syndromes such as cancer, bacterial, viral or parasitic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited genetic diseases). The present sequence represents a targeting factor for lipid-nucleic acid complexes of the invention
 Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
 Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
 Lipid-nucleic acid complex; polycation; targeting factor; gene therapy; cancer; infection; immune deficiency; gene defect; genetic disease;
 Gaps
 ö
 Amino acid sequence of membrane translocating peptide Elan094.
 specification describes a lipid-nucleic acid complex,
 6; Length 15;
 1; Indels
 Score 51; DB 6;
Pred. No. 0.15;
 O'mahony DJ;
 Mismatches
 Disclosure; Page 42; 259pp; English.
 Disclosure; Page 10; 259pp; English.
 ABP70214 standard; peptide; 15 AA.
 (TARG-) TARGETED GENETICS CORP.
(EMER-) EMERALD GENE SYSTEMS LTD.
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 membrane translocating peptide.
 Cudmore S,
 30-APR-2002; 2002WO-US013609.
 30-APR-2001; 2001US-0287786P.
 67.1%;
 (first entry)
 KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 Local Similarity 92.3
es 12; Conservative
 WPI; 2003-183837/18.
 WPI; 2003-183837/18
 Paul R,
 Sequence 15 AA;
 WO200288318-A2
 Unidentified
 07-APR-2003
 07-NOV-2002
 Harvie P,
 ABP70214;
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 Query Match
 Matches
 RESULT 13
g
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The specification describes a lipid-nucleic acid complex, comprising a

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 The specification describes a lipid-nucleic acid complex, comprising a compacted nucleic acid, a polycation, a targeting factor and a lipid, but not a protramine. The targeting factor increases cellular bioavailability of the nucleic acid without interaction with a specific outer cell surface membrane receptor. The mean diameter of the complex is greater
compacted nucleic acid, a polycation, a targeting factor and a lipid, but not a protamine. The targeting factor increases cellular bicavailability of the nucleic acid without interaction with a specific outer cell surface membrane receptor. The mean diameter of the complex is greater than 100 nm and less than 400 nm. The lipid-nucleic acid complex is useful for delivering a nucleic acid to a cell in vivo, e.g. for gene therapy. It reduces levels of inflammatory cytokines such as tumour necrosis factor-alpha. The complex is useful for manufacturing a necionant for treating or diagnosing a variety of diseases, conditions or syndromes such as cancer, bacterial, viral or parasitic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited genetic diseases). The present sequence represents a membrane nucleic acid complexes of the invention
 Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
 Lipid-nucleic acid complex; polycation; targeting factor; gene therapy; cancer; infection; immune deficiency; gene defect; genetic disease.
 Gaps
 ö
 Score 51; DB 6; Length 15; Pred. No. 0.15;
 1, Indels
 Amino acid sequence of targeting factor Elan094G.
 Harvie P, Paul R, Cudmore S, O'mahony DJ;
 /note= "galactose attached"
 0; Mismatches
 /note= "Des-Pro attached"
 Disclosure, Page 42; 259pp; English.
 Location/Qualifiers
 ABP70233 standard; peptide; 15 AA.
 (EMER-) EMERALD GENE SYSTEMS LTD
 (TARG-) TARGETED GENETICS CORP
 30-APR-2001; 2001US-0287786P.
 67.1%;
92.3%;
 30-APR-2002; 2002WO-US013609.
 (first entry)
 S KAAAAVLLPVLLA 17
 Local Similarity 92.3
hes 12, Conservative
 WPI; 2003-183837/18.
 Sequence 15 AA;
 WO200288318-A2
 Modified-site
 Modified-site
 Unidentified
 07-APR-2003
 07-NOV-2002.
 ABP70233;
 Query Match
 Matches
 88888888888888888888888888888888888
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Sequence 15 AA;

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than 100 nm and less than 400 nm. The lipid-nucleic acid complex is useful for delivering a nucleic acid to a cell in vivo, e.g. for gene therapy. It reduces levels of inflammatory cytokines such as tumour necrosis factor-alpha. The complex is useful for manufacturing a medicament for treating or diagnosing a variety of diseases, conditions or syndromes such as cancer, bacterial, viral or parasitic infections, immune deficiencies, gene defects, and gene deficiencies (e.g. inherited genetic diseases). The present sequence represents a targeting factor for lipid-nucleic acid complexes of the invention
 888888888888888
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Sequence 15 AA;

Gaps ö Score 51, DB 6; Length 15; Pred. No. 0.15; 0; Mismatches 1; Indels 1; Indels 67.18; Query Match
Best Local Similarity 92.3
Matches 12, Conservative

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S KAAAAVLLPVLLA 17 

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ABG75426 standard; peptide; 15 AA. ABG75426; RESULT 15 ABG75426 

Membrane translocating peptide #1. (first entry) 15-APR-2004

peptide; transmembrane transport; gastrointestinal tract. note= "modified by epsilon-dansyl" Location/Qualifiers Membrane translocating enzymatic degradation; modified_site modified_site Unidentified Key

WO2003089458-A2

/note= "C-terminal amide"

30-OCT-2003

21-APR-2003; 2003WO-US012543

19-APR-2002; 2002US-00126845.

(SARL-) SARLAN LTD.

Composition, useful for treating a pathological disease in an animal, comprises a transport peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment

Pinilla C;

Houghten R,

Lambkin I,

O'mahony DJ,

WPI; 2004-034528/03.

Claim 1; Page 24; Opp; English.

The present invention relates to a composition which comprises a translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment of at least 4 amino acids of the transport peptide. The composition is useful in treating a pathological disorder in an animal, as it protects an orally delivered active agent from enzymatic degradation in the gastrointestinal tract (GIT), and promotes absorption across epithelial cells lining the GIT. The present sequence is a polypeptide used in the exemplification of the invention

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 Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system; targeting peptide.
 Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic
 Gaps
 ö
 Length 15;
 Indels
 'note= "N-terminus has a dansyl group'
 Score 51; DB 8;
Pred. No. 0.15;
 Mismatches
 /note= "C-terminal amide"
 Human targeting peptide sequence #1.
 Location/Qualifiers
 Ė
 ;
0
 AAU00655 standard; peptide; 19
 67.1%;
92.3%;
 27-SEP-2000; 2000WO-IB001491
 99US-0156246P
 (first entry)
 KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 O'mahony DJ, Lambkin IJ;
 Conservative
 (OMAH/) O'MAHONY D J.
(LAMB/) LAMBKIN I J.
 WPI; 2001-300212/31.
 WO200127154-A2
 Key
Modified-site
 Modified-site
 Homo sapiens.
 27-SEP-1999;
 07-SEP-2001
 19-APR-2001
 AAU00655;
 RESULT 16
```

The sequence represents a human targeting peptide which is used to identify the presence of a human membrane translocated peptide (WTLP) and quantify the amount, to bind the WTLP to the surface of a particle, or to localise the WTLP in a cell or tissue sample. WTLPs and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer lining the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle, into the circulatory system of an animal. This method for the identification of WTLPs which retain the functional activity of a full-length WTLP, as a cell-based screen for assaying the functional activity of a MTLP, as a characterising the properties of a MTLP, for diagnosis of a pathological disorder. (by administration of a MTLP, for diagnosis of a pathological disorder particle complex comprising a diagnostic agent) and for preventing or treating a pathological disorder. 

Example 1; Page 22; 42pp; English.

acid sequences of the peptides.

Sequence 19 AA;

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ADB88777 standard; peptide; 19 AA.
 ADB88777;
 invention
 Query Match
 factor.
 RESULT 18
 ADB8877
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 The sequence represents a human membrane translocated peptide (WTLP).

WTLPS and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer lining the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle, into the dircularcy system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the demtification of MTLP which retain the functional activity of a MTLP, as a cell-based screen for assaying the functional activity of a MTLP and characterising the properties of a MTLP. for diagnosis of a pathological disorder (by administration of a MTLP-active agent complex or myTLP-active particle complex comprising a diagnostic agent) and for the preventing or treating a pathological disorder
 ö
 Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic of the peptides.
 Membrane translocating peptide, MTLP, human, intracellular gene delivery, epithelial cell layer, gastrointestinal tract, circulatory system.
 Gaps
 .
0
Score 51; DB 4; Length 19;
Pred. No. 0.19;
0; Mismatches 1; Indels
 Score 51; DB 4; Length 19;
Pred. No. 0.19;
0; Mismatches 1; Indels
 Human membrane translocating peptide (MTLP) #3.
 AAU00634 standard; peptide; 19 AA.
 Claim 2; Page 11; 42pp; English.
 67.1%;
 27-SEP-2000; 2000WO-IB001491.
 99US-0156246P.
 67.1%;
ilarity 92.3%;
Conservative
 (first entry)
 5 KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 O'mahony DJ, Lambkin IJ;
 Best Local Similarity 92.
 (OMAH/) O'MAHONY D J. (LAMB/) LAMBKIN I J.
 WPI; 2001-300212/31.
 N-PSDB; AAS00628
 Sequence 19 AA;
 WO200127154-A2.
 Homo sapiens.
 27-SEP-1999;
 07-SEP-2001
 19-APR-2001
 AAU00634;
 Query Match
 Query Match
 RESULT 17
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The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mRNA is greater than in a non-Peyer's patch cell. The preferred protein of the cinvention is a transcription factor or a protein that activates a stranscription factor selected from Jun-B, c-jun related TF, Jun-D, STAT 3 consoling transfaucer and activator of transcription 3, Nfkappa&bgr; Tf plos subunit, S-myc prote-oncogene, myc related, Nm21-M2, nucleoside ciphosphate kinase B, metastasis reducing protein, and C-est-I protoconcogene, and p54. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein CD5 precursor. HSP concogene, and p54. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein CD5 precursor. HSP concogene, and p64. The preferred upregulated protein protein is selected from the group. The method is useful for increasing or protein selected from the group. The method is useful for increasing or decreasing the level of a protein in a Peyer's patch cell, particularly in increasing antigen or vaccine delivery to M cells. The method may also be used to enhance transport of a drug through the gastrointestinal tract increasing content increasing peptide of the increasing peptide of the increasing protein in a membrane translocating peptide of the
 Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
 Gaps
 Peyer's patch cell; non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell; membrane translocating peptide.
 ô
 Length 19;
 1; Indels
 Score 51; DB 7;
Pred. No. 0.19;
 0; Mismatches
 Example 6; Page 51; 147pp; English.
 Brayden D;
 ABG75428 standard; peptide; 19 AA.
 Membrane translocating peptide #3.
 04-APR-2002; 2002WO-IB003866.
 04-APR-2001; 2001US-0281387P.
 67.1%;
92.3%;
04-DEC-2003 (first entry)
 KKAAAVLEPVLLA 13
 S KAAAAVLLPVLLA 17
 Best Local Similarity 92.3
Matches 12; Conservative
 O'mahony DJ, Byrne D,
 (OMAH/) O'MAHONY D J.
 WPI; 2003-229409/22.
 WO2003004646-A2
 Sequence 19 AA;
 Unidentified.
 16-JAN-2003.
 RESULT 19
ABG75428
ID ABG75
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Gaps

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KAAAAVLLPVLLA 17

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Local Similarity es 12; Conserv

Best Loc Matches

1 KKAAAVLLPVLLA 13

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Best Local Similarity
 N-PSDB; AAS00626
 Sequence 21 AA;
 WO2003004646-A2
 WO200127154-A2
 Homo sapiens.
 27-SEP-1999;
 Unidentified
 16-JAN-2003.
 19-APR-2001.
 ADB88775;
 Query Match
 (LAMB/)
 Matches
 RESULT 21
 ADB88775
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 ö
 Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
 Composition, useful for treating a pathological disease in an animal, comprises a translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active
 The present invention relates to a composition which comprises a transport peptide, an extended translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment of at least 4 amino acids of the transport peptide. The composition is useful in treating a pathological disorder in an animal, as it protects an orally delivered active agent from enzymatic degradation in the gastrointestinal tract (GIT), and promotes absorption across epithelial cells liming the GIT. The present sequence is a polypeptide used in the
 Gaps
 ;
 Score 51; DB 8; Length 19;
Pred. No. 0.19;
0; Mismatches 1; Indels
 Membrane translocating peptide; transmembrane transport;
 'note= "modified by epsilon-dansyl"
 O'mahony DJ, Lambkin I, Houghten R, Pinilla C;
 Human membrane translocating peptide (MTLP) #1.
 enzymatic degradation; gastrointestinal tract
 /note= "C-terminal amide"
 Location/Qualifiers
 AAU00632 standard; peptide; 21 AA.
 Membrane translocating peptide #3
 exemplification of the invention
 Claim 1; Page 24; Opp; English.
 21-APR-2003; 2003WO-US012543.
 19-APR-2002; 2002US-00126845
 Match 67.1%;
Local Similarity 92.3%;
les 12; Conservative
 (first entry)
 5 KAAAAVLLPVLLA 17
 1 KKAAAVLLPVLLA 13
 WPI; 2004-034528/03.
 (SARL-) SARLAN LTD
 WO2003089458-A2
 Sequence 19 AA;
 Key
modified_site
 modified_site
 Unidentified
 15-APR-2004
 30-0CT-2003
 ABG75428;
 fragment.
 AAU00632;
 Query Match
 Best Loca
Matches
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 Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic of the peptides.
 The sequence represents a human membrane translocated peptide (MTLP). MTLPs and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer example, an epithelial cell layer lining the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle, into the circulatory system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the identification of MTLPs which retain the functional activity of a full-length MTLP, as a cell-based screen for assaying the functional activity of a MTLP and characterising the properties of a MTLP. for diagnosis of a pathological disorder (by administration of a MTLP, for diagnosis of a pathological disorder (by administration of a MTLP-active agent complex or MTLP-active agent complex or MTLP-active agent and for
 Gaps
 Peyer's patch cell; non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell; membrane translocating peptide.
 ö
 Score 51; DB 4; Length 21; Pred. No. 0.22; 0; Mismatches 1; Indels
 preventing or treating a pathological disorder
 Membrane translocating peptide #1.
 ADB88775 standard; peptide; 21 AA.
 Claim 1; Page 11; 42pp; English.
27-SEP-2000; 2000WO-IB001491
 99US-0156246P
 67.18;
 04-APR-2002; 2002WO-IB003866.
 04-DEC-2003 (first entry)
 ij
 S KAAAAVLLPVLLA 17
 12; Conservative
 O'mahony DJ, Lambkin
 (OMAH/) O'MAHONY D J.
 LAMBKIN I J.
 WPI; 2001-300212/31.
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The present invention describes a cell permeable peptide comprising at least the hydrophobic core of a signal peptide (or analogue) containing at least that additional positively charged amino acid (or analogue). The peptides are useful for the intracellular delivery of molecules, especially peptide nucleic acids to in vivo targets. The peptides are useful in commercial drug-delivery systems, in e.g. gene therapy, cancer therapy and anti-infectious agent therapy. The peptides facilitate biochemical and molecular biological research. The modified peptides facilitate intracellular delivery of any cell-impermeable substances and improve delivery into low permeablity calls. Delivery into sub-compartments can be achieved by modifying the signal peptides. The present sequence represents a peptide used in the exemplification of the
 New cell permeable signal peptides, useful for intracellular delivery of
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 131.
 C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 Length 22;
 3; Indels
 67.1%; Score 51; DB 3; 70.6%; Pred. No. 0.23; ive 2; Mismatches
 Borrello MA;
 ä
 ADK50919 standard; peptide; 21 AA.
 Example 4; Fig 6; 33pp; English.
 Wallace
 ||||:||| |:|
KKKKKAAVALLPAVLLA 18
 1 KKKRKAAAAVLLPVLLA 17
 10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
 10-JUN-2003; 2003WO-US018252.
98GB-00012376
98GB-00014888
 (UYBE-) UNIV QUEENS BELFAST.
 (first entry)
 Query Match
Best Local Similarity 70.6'
Matches 12; Conservative
 (VACC-) VACCINEX INC. (UYRP) UNIV ROCHESTER.
 Harriott P,
 Evans EE,
 WPI; 2004-062349/06.
 WPI; 2000-097517/Q8
 present invention
 WO2003104428-A2.
 Sequence 22 AA;
10-JUN-1998;
 10-JUL-1998;
 04-NOV-2004
 Unidentified
 sapiens
 Zauderer M,
 18-DEC-2003.
 molecule
 Nelson J,
 ADK50919;
 RESULT 23
 ADK50919
##X#X#X#X###X#X##X
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 The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mana is greater than in a non-Peyer's patch cell. The preferred protein of the invention is a transcription factor or a protein that activates a transcription factor or a protein that activates a signal transducer and activator of transcription 3, NKAspasabgr; Tf plos subunit, S-myc proto-oncogene, myc related, Nm23-M2, nucleoside and p54. The preferred upregulated protein, and C-est-I proto-oncogene, and p54. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein of the invention is selected from the group. The method is useful for increasing or decreasing the level of a protein in a Peyer's patch cell, particularly in increasing antigen or vaccine delivery to M cells. The method any also be used to enhance transport of a drug through the gastrointestinal traction in the companies.
 ö
 Increasing the levels of a protein in a Peyer's patch cell, useful for cargeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
 Karposi syndrome fibroblast growth factor modified signal peptide #5.
 Gaps
 Karposi syndrome, fibroblast growth factor, signal peptide, PNA,
peptide nucleic acid, cell permeability, intracellular delivery,
 ö
 /note= "labelled with carboxyfluorescein"
 DB 7; Length 21;
 1; Indels
 Score 51; DB 7
Pred. No. 0.22;
0; Mismatches
 Location/Qualifiers
 Example 6; Page 51; 147pp; English.
 Brayden D;
 AAY67959 standard; peptide; 22 AA.
 ..
04-APR-2001; 2001US-0281387P.
02-JUL-2001; 2001US-0302591P.
 99WO-GB001848
 67.1%;
 92.3%;
 05-APR-2000 (first entry)
 S KAAAAVLLPVLLA 17
 Query Match
Best Local Similarity 92.3
Matches 12; Conservative
 à
 gene therapy; cancer.
 (OMAH/) O'MAHONY D J.
 Byrne
 WPI; 2003-229409/22.
 Sequence 21 AA;
 Key
Modified-site
 10-JUN-1999;
 Homo sapiens
 W09964449-A2
 16-DEC-1999
 invention.
 Synthetic.
 O'mahony
 targeted
 AAY67959;
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Gaps

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us-10-764-235-24.rag

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 The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 132.
C35 polypeptide useful for formulation of immunogenic composition duce antibodies and cell-mediated immunity against tumor cells.
 Gaps
 C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 ö
 DB 8; Length 21;
 2; Indels
 Score 50; DB 8;
Pred. No. 0.31;
0; Mismatches
 Disclosure; Page 225; 626pp; English.
 Borrello MA;
 ADK50920 standard; peptide; 33 AA
 10-JUN-2002; 2002US-038673BP
11-DEC-2002; 2002US-0432241P
23-APR-2003; 2003US-0464650P.
 65.8%;
 10-JUN-2003; 2003WO-US018252
 17
 Query Match
Best Local Similarity 85...
Best Local 12; Conservative
 04-NOV-2004 (first entry)
 4 RKAAAAVLLPVLLA
 Evans EE,
 (VACC-) VACCINEX INC. (UYRP) UNIV ROCHESTER
 WPI; 2004-062349/06.
 WO2003104428-A2.
 Sequence 21 AA;
 Unidentified.
 sapiens
 Zauderer M,
 18-DEC-2003,
 ADK50920;
 Novel
 Homo
 RESULT 24
 ADK50920
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The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder

Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.

Disclosure; Page 225; 626pp; English.

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The present invention describes an isolated PRO nucleic acid (I). Also described: (I) a vector comprising (I); (2) a host cell comprising the vector of (I); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimaric molecule comprising the colypeptide of (4) fused to a heterologous amino acid sequence; (6) an antipody which specifically binds to a polypeptide of (4), (7) a composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the composition of antagonist of the polypeptide or an antibody that binds to the composition of antagonist of the polypeptide or an antibody that binds to the comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal, (10) a method for determining the presence of a PRO polypeptide; (II) a method of diagnosing an immune response in mammal; (12) a method of identifying a compound that inhibits or
 human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiasthmatic; antidiabetic; antinflammatory; antipsoriatic; antirhyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
 New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Gaps
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 Schoenfeld J, Williams PM;
 Length 33
 2; Indels
 .,
8
 Score 50; DB 8
Pred. No. 0.5;
 0; Mismatches
 Human PRO protein sequence SEQ ID NO:350.
 Claim 1; SEQ ID NO 350; 3009pp; English.
 ADP54374 standard; protein; 433 AA.
 Gurney AL,
 stimulating an immune response.
 28-OCT-2003; 2003WO-US034381.
 65.8%;
85.7%;
 29-OCT-2002; 2002US-0422472P
 4 RKAAAAVLLPVLLA 17
 18-NOV-2004 (first entry)
 12, Conservative
 virucide; gene therapy.
 3, Clark H,
Wu TD;
 (GETH) GENENTECH INC
 WPI; 2004-376182/35.
N-PSDB; ADP54373.
 Query Match
Best Local Similarity
 Sequence 33 AA;
 WO2004039956-A2
 Homo sapiens.
 13-MAY-2004.
 Aggarwal S,
 ADP54374;
 18
 Wood WI,
 Matches
 RESULT 25
 ADP5437
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 polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, esteopathic, antidiabetic, dermatological, antiporitatic, antiallergic, antiathmatic, hepatotropic, and respiratory activity. A polymucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, iuvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
mimics the activity of or expression of a gene encoding a PRO polypeptide pro sequences have antialtergic, antianemetic, antiarthritic, antiatehmenic, antiatheric, antiarthritic, antiathemetic, antithyroid, CNS, dermatological, gastrointestinal, haemostatic, hepatotropic, immunostimularic, immunostipressive, muscular, nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid virucide activities, and can be used in gene therapy. The nucleic acid useful in diagnosing and treating an immune response. The present sequence represents a human PRO protein from the present invention.
 New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.
 PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
 Gaps
 The invention relates to a novel isolated nucleic acid and the PRO
 Williams PM, Wood WI;
 ö
 8; Length 433;
 1; Indels
 DB
16;
 Mismatches
 Van Lookeren M,
 Claim 7; SEQ ID NO 580; 2940pp; English.
 63.2%; Score 48; 60.0%; Pred. No.
 ADP23402 standard; protein; 433 AA.
 <u>ن</u>
 PRO polypeptide SEQ ID NO:580.
 30-OCT-2003; 2003WO-US034312.
 01-NOV-2002; 2002US-0423394P
 1 KKKRKAAAAVLLPVL 15
 :::|:||| :|||||
RRRRRAAAPLLLPVL 20
 (first entry)
 Best Local Similarity 60.0
Matches 9; Conservative
 Schoenfeld J,
 (GETH) GENENTECH INC
 WPI; 2004-419628/39.
 N-PSDB; ADP23401
 Sequence 433 AA;
 WO2004041170-A2
 Unidentified
 18-NOV-2004
 21-MAY-2004.
 ADP23402;
 Clark H,
 Query Match
 Wu TD;
 RESULT 26
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consisting autoimmatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune chrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polymeuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polymeuropathy, Guillain-Barre syndrome, consease, infectious or autoimmune chronic active hepatitis, primary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's consease, an autoimmune or immune-mediated skin disease, authorism and cliecase, active mediate a syndrome, consease, a bullous skin cliecase, asthma, allergic rhinitis, atopic dermatitis, food disease, asthma, allergic rhinitis, atopic dermatitis, food consensitivity utticaria, an immunologic disease of the lung, consinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity prefers a transplantation associated disease, graft rejection or consinophic process. The present sequence represents a PRO protein
 ö
 Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic
 Membrane translocating peptide; MTLP; human, intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
 The sequence represents a human membrane translocated peptide (MTLP). MTLPs and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer lining the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle,
 Gaps
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 8; Length 433;
 1; Indels
 Human membrane translocating peptide (MTLP) #6.
 8
 5; Mismatches
 Score 48; DB
Pred. No. 16;
 AAU00637 standard; peptide; 14 AA
 Claim 2; Page 11; 42pp; English.
 27-SEP-2000; 2000WO-IB001491.
 99US-0156246P
 63.2%;
 RRRRRAAAPLLLPVL 20
 1 KKKRKAAAAVLLPVL 15
 (first entry)
 O'mahony DJ, Lambkin IJ;
 9; Conservative
 (OMAH/) O'MAHONY D J.
 WPI; 2001-300212/31.
 (LAMB/) LAMBKIN I J.
 Local Similarity
 of the invention.
 N-PSDB; AASO0631
 the peptides.
 Sequence 433 AA;
 WO200127154-A2.
 27-SEP-1999;
 Homo sapiens,
 07-SEP-2001
 19-APR-2001.
 AAU00637;
 Query Match
 Matches
 RESULT 27
 AAU00637
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The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mana is greater than in a non-Peyer's patch cell. The preferred protein of the invention is a transcription factor or a protein that activates a transcription factor selected from Jun-B, c-jun related TF, Jun-D, STAT 3 -signal transducer and activator of transcription 3, NKtappakbgr; Tf plo5 subunit, S-myc proto-oncogene, myc related, Nm23-M2, nucleoside diphosphate kinase B, metagrasis reducing protein, and C-est-I proto-oncogene, and p54. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface 9lycoprotein CD5 precursor, HSP selected from clusterin, T-cell surface 9lycoprotein CD5 precursor, HSP selected from the group. The method is useful for increasing or decreasing the level of a protein in a Peyer's patch cell, particularly in increasing antigen or vaccine delivery to M cells. The method may also
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 intracellular gene delivery, as a rapid screening method for the dentification of MTLPs which retain the functional activity of a full-length MTLP, as a cell-based screen for assaying the functional activity of a MTLP, and characterising the properties of a MTLP, for diagnosis of a pathological disorder (by administration of a MTLP-active agent complex or MTLP-active particle complex comprising a diagnostic agent) and for preventing or treating a pathological disorder
 Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
 Gaps
into the circulatory system of an animal. This method is useful for
 Peyer's patch cell; non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell; membrane translocating peptide.
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 Score 47; DB 4; Length 14;
Pred. No. 0.64;
0; Mismatches 2; Indels
 Example 6; Page 51; 147pp; English
 ADB88780 standard; peptide; 14 AA
 Brayden D;
 Membrane translocating peptide #6.
 04-APR-2002; 2002WO-IB003866
 04-APR-2001; 2001US-0281387P. 02-JUL-2001; 2001US-0302591P.
 Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
 (first entry)
 5 KAAAAVLLPVLLA 17
 1 KKCAAVLLPVLLA 13
 O'mahony DJ, Byrne D,
 (OMAH/) O'MAHONY D J.
 WPI; 2003-229409/22.
 WO2003004646-A2.
 Sequence 14 AA;
 Unidentified
 04-DEC-2003
 16-JAN-2003
 ADB88780;
 RESULT 28
 ADB88780
 8X33333333X8
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 an
 The present invention relates to a composition which comprises a translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment of at least 4 amino acids of the transport peptide. The composition is useful in treating a pathological disorder in an animal, as it protects an orally delivered active agent from enzymatic degradation in the gastrointestinal tract (GIP), and promotes absorption across epithelial cells liming the GIT. The present sequence is a polypeptide used in the
 Composition, useful for treating a pathological disease in an animal, comprises a transport peptide, are extended peptide comprising the transport peptide or a transport-active
sed to enhance transport of a drug through the gastrointestinal traverins sequence represents a membrane translocating peptide of the
 Gaps
 Gaps
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 ö
 Length 14;
 Length 14
 2; Indels
 Membrane translocating peptide; transmembrane transport; enzymatic degradation; gastrointestinal tract.
 Indels
 Ü
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 Pinilla
 61.8%; Score 47; DB 8;
100.0%; Pred. No. 0.64;
:ive 0; Mismatches
 DB 7;
 0; Mismatches
 /note= "C-terminal amide"
 Score 47;
Pred. No.
 Houghten R,
 Location/Qualifiers
 Membrane translocating peptide #2.
 ABG75427 standard; peptide; 14 AA.
 exemplification of the invention
 Claim 1; Page 24; Opp; English.
 21-APR-2003; 2003WO-US012543
 19-APR-2002; 2002US-00126845.
 61.8%;
84.6%;
 (first entry)
 13
 1 KKCAAVLLPVLLA 13
 Lambkin I,
 11; Conservative
 11; Conservative
 17
 5 KAAAAVLLPVLLA
 7 AAAVLLPVLLA
 WPI; 2004-034528/03.
 Query Match
Best Local Similarity
 (SARL-) SARLAN LTD
 Local Similarity
 Sequence 14 AA;
 WO2003089458-A2
 Sequence 14 AA;
 modified site
 O'mahony DJ,
 15-APR-2004
 Unidentified
 30-0CT-2003
 used to
 invention.
 ABG75427;
 fragment.
 Query Match
 (GIL)
 Matches
 RESULT 29
 Matches
 ABG75427
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ABG75431 RESULT

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The sequence represents a human membrane translocated peptide (WTLP).

WILPS and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer lining the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle, into the circulatory system of a naimal. This method is useful for intracellular gene delivery, as a rapid screening method for the identification of WTLPs which retain the functional activity of a full-length MTLP, as a cell-based screen for assaying the functional activity of a pathological disorder (by administration of a WTLP-active agent complex or MTLP-active particle complex comprising a diagnostic agent) and for preventing or treating a pathological disorder
 Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic
 Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
 Peyer's patch cell; non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell; membrane translocating peptide.
 ö
 Score 47; DB 4; Length 16;
 2; Indels
 membrane translocating peptide (MTLP) #4.
 Pred. No. 0.74;
0; Mismatches
 Membrane translocating peptide #4.
 ADB88778 standard; peptide; 16 AA.
 Claim 2; Page 11; 42pp; English.
 99US-0156246P.
 27-SEP-2000; 2000WO-IB001491
 61.8%;
 (first entry)
 S KAAAAVLLPVLLA 17
 KKCAAVLLPVLLA 13
 O'mahony DJ, Lambkin IJ;
 11; Conservative
 (OMAH/) O'MAHONY D J.
 (LAMB/) LAMBKIN I J.
 WPI; 2001-300212/31.
 Best Local Similarity
 N-PSDB; AAS00629
 the peptides.
 Sequence 16 AA;
 WO200127154-A2
 Homo sapiens
 27-SEP-1999;
 04-DEC-2003
 Unidentified
 19-APR-2001.
 ADB88778;
 Query Match
 Human
 Matches
 ADB88778
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 translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment of at least 4 amino acids of the transport peptide. The composition is useful in treating a pathological disorder in an animal, as it protects an orally delivered active agent from enzymatic degradation in the gastrointestinal tract (GIT), and promotes absorption across epithelial cells liming the GIT. The present sequence is a polypeptide used in the exemplification of the invention
 Composition, useful for treating a pathological disease in an animal, comprises a transport peptide, are extended peptide comprising the transport peptide or a transport-active
 Gaps
 The present invention relates to a composition which comprises a
 ö
 Length 14;
 2; Indels
 Membrane translocating peptide; transmembrane transport; enzymatic degradation; gastrointestinal tract.
 'note= "modified by epsilon-dansyl"
 Pinilla C;
 DB 8;
 Pred. No. 0.64;
; Mismatches
 /note= "C-terminal amide"
 Score 47;
 Houghten R,
 Location/Qualifiers
 Membrane translocating peptide #6.
 AAU00635 standard; peptide; 16 AA.
 ABG75431 standard; peptide; 14 AA
 ;
 Claim 1; Page 24; Opp; English.
 21-APR-2003; 2003WO-US012543.
 19-APR-2002; 2002US-00126845
 61.8%;
 Local Similarity 84.6%;
nes 11; Conservative
 15-APR-2004 (first entry)
 (first entry)
 1 KKCAAVLLPVLLA 13
 S KAAAAVLLPVLLA 17
 Lambkin I,
2 AAAVLLPVLLA 12
 WPI; 2004-034528/03.
 (SARL-) SARLAN LTD.
 WO2003089458-A2
 Sequence 14 AA;
 modified_site
 modified_site
 O'mahony DJ,
 Unidentified
 07-SEP-2001
 ABG75431;
 AAU00635;
 Query Match
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Gaps

Best Loca Matches

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RESULT 31 AAU00635

SXE

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New peptidomimetic compounds are tumor cell replication inhibitors useful to treat tumors or oncological disorders of e.g. breast, kidney, mouth, larynx, esophagus, stomach, testis, cervix, head, neck, colon, ovary,
 Composition, useful for treating a pathological disease in an animal, comprises a transport peptide, ar extended peptide comprising the transport peptide or a transport-active
 The present invention relates to a composition which comprises a translocating peptide, consisting of a transport peptide, an extended peptide comprising the transport peptide or a transport-active fragment of at least 4 amino acids of the transport peptide. The composition is useful in treating a pathological disorder in an animal, as it protects an orally delivered active agent from enzymatic degradation in the gastrointestinal tract (GIT), and promotes absorption across epithelial cells lining the GIT. The present sequence is a polypeptide used in the exemplification of the invention
 Gaps
 peptidomimetic; Cytostatic; Tumour; Apoptosis; oncological disorder.
 ö
 Length 16;
 2; Indels
 Peptide comprising a membrane translocating sequence #2.
 Pinilla C;
 Score 47; DB 8;
Pred. No. 0.74;
 Hamilton AD
 0; Mismatches
 Houghten R,
 ADR40510 standard; peptide; 18 AA.
 Claim 1; Page 24; Opp; English.
 Sebti SM,
 19-APR-2002; 2002US-00126845.
 21-APR-2003; 2003WO-US012543
 61.8%;
84.6%;
 20-FEB-2004; 2004WO-US005030.
 20-FEB-2003; 2003US-0319960P.
 (UYSF-) UNIV SOUTH FLORIDA.
 18-NOV-2004 (first entry)
 1 KKCAAVLLPVLLA 13
 Lambkin I,
 5 KAAAAVLLPVLLA 17
 11; Conservative
 WPI; 2004-034528/03.
 Turkson J, Jove R,
 WPI; 2004-642398/62.
 (SARL-) SARLAN LTD.
 Best Local Similarity
 WO2003089458-A2.
 WO2004073650-A2
 Sequence 16 AA;
 Б,
 Unidentified
 30-0CT-2003
 02-SEP-2004.
 O'mahony
 Query Match
 Matches
 ò
 The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mkNA is greater than in a non-Peyer's patch cell. The preferred protein of the invention is a transcription factor or a protein that activates a circuit ranscription factor selected from Jun-B, c-jun related TF, Jun-D, STAT 3 - eignal transducer and activator of transcription 3, NKappababyr; Tf plos subunit, S-myc proto-oncogene, myc related, NM3-M2, nucleoside diphosphate kinase B, metastasis reducing protein, and C-est-I proto-concogene, and p54. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein of precursor, HSP 84, and Ca2+ dependent phospholipase A2 precursor and the mRNA is for a protein selected from the group. The method is useful for increasing or protein selected from the group. The method is useful for increasing or decreasing the level of a protein in a Peyer's patch cell, particularly in increasing antigen or vaccine delivery to M cells. The method may also be used to enhance transport of a drug through the gastrointestinal tract for increasing contents. This sequence represents a membrane translocating peptide of the
 ó,
 Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
 Gaps
 ;
0
 Score 47; DB 7; Length 16;
 2; Indels
 Membrane translocating peptide; transmembrane transport; enzymatic degradation; gastrointestinal tract.
 /note= "modified by epsilon-dansyl"
 Pred. No. 0.74
0; Mismatches
 /note= "C-terminal amide"
 Location/Qualifiers
 Example 6; Page 51; 147pp; English.
 Brayden D;
 ABG75429 standard; peptide; 16 AA.
 Membrane translocating peptide #4.
 04-APR-2002; 2002WO-IB003866;
 02-JUL-2001; 2001US-0302591P
 61.8%;
 (first entry)
 5 KAAAAVLLPVLLA 17
 KKCAAVLLPVLLA 13
 Local Similarity 84.6
 O'mahony DJ, Byrne D,
 (OMAH/) O'MAHONY D J.
 WPI; 2003-229409/22.
WO2003004646-A2
 Sequence 16 AA;
 Key
modified_site
 modified_site
 04-APR-2001;
 Unidentified
 15-APR-2004
 16-JAN-2003
 ABG75429;
 Query Match
 Best Loca
Matches
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ઠે 요 Gaps

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Indels

5

Matches

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RESULT 35

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The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Novel C15 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 19.
 C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 61.8%; Score 47; DB 8; Length 21; 91.7%; Pred. No. 0.98; 1; Indels ive 0; Mismatches 1; Indels
 Pred. No. 0.84;
0; Mismatches
 Disclosure; Page 197; 626pp; English.
 Borrello MA;
 ADK50911 standard; peptide; 21 AA.
 ADK50807 standard; peptide; 21 AA.
 11-DEC-2002; 2002US-0432241P. 23-APR-2003; 2003US-0464650P.
 10-JUN-2003; 2003WO-US018252
 10-JUN-2002; 2002US-0386738P
 84.68;
 (first entry)
 S KAAAAVLLPVLLA 17
 11; Conservative
 6 AAAAVLLPVLLA 17
 Conservative
 VACCINEX INC.
UNIV ROCHESTER.
 Zauderer M, Evans EE,
 WPI; 2004-062349/06.
Best Local Similarity
Matches 11; Conserv
 Similarity
 WO2003104428-A2.
 Sequence 21 AA;
 Homo sapiens
Unidentified
 04-NOV-2004
 18-DEC-2003
 ADK50807;
 Query Match
 (VACC-)
 Local
 UYRP)
 RESULT 37
 ADK50911
ID ADK5
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 RESULT 34
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 New peptidomimetic compounds are tumor cell replication inhibitors useful to treat tumors or oncological disorders of e.g. breast, kidney, mouth, larynx, esophagus, stomach, testis, cervix, head, neck, colon, ovary, lung, bladder and skin.
 The present invention relates to peptidomimetic compounds and their salts. The compound is useful in the treatment of a tumour or an oncological disorder (breast, kidney, mouth, larynx, oesophagus, stomach, testis, cervix, head, neck, colon, ovary, lung, bladder, skin, muscle, pancreas, prostate, bone, eye, blood cells or brain cancers) in a human or animal. The present sequence represents is a peptide comprising a membrane translocating sequence.
 salts. The compound is useful in the treatment of a tumour or an oncological disorder (breast, kidney, mouth, larynx, oesophagus, stomach, testis, cervix, head, neck, colon, ovary, lung, bladder, skin, muscle, pancreas, prostate, bone, eye, blood cells or brain cancers) in a human or animal. The present sequence represents is a peptide comprising a membrane translocating sequence.
 Gaps
 peptidomimetic; Cytostatic; Tumour; Apoptosis; oncological disorder.
 The present invention relates to peptidomimetic compounds and their
 ö
 Length 18;
 Score 47; DB 8; Length 18; Pred. No. 0.84;
 2; Indels
 Peptide comprising a membrane translocating sequence #1.
 DB 8;
 Hamilton AD;
 0; Mismatches
 /note= "phosphorylated"
 61.8%; Score 47;
 Example 3; SEQ ID NO 1; 47pp; English
 Example 5; SEQ ID NO 2; 47pp; English.
 Location/Qualifiers
2
 ADR40509 standard; peptide; 18 AA.
 Jove R, Sebti SM,
 61.8%;
84.6%;
 20-FEB-2004; 2004WO-US005030
 20-FEB-2003; 2003US-0319960P
 (UYSF-) UNIV SOUTH FLORIDA
 4 KTKAAVLLPVLLA 16
 (first entry)
 5 KAAAAVLLPVLLA 17
 11; Conservative
 lung, bladder and skin.
 WPI; 2004-642398/62.
 Query Match
Best Local Similarity
 WO2004073650-A2
 Sequence 18 AA;
 Sequence 18 AA;
 Key
Modified-site
 Unidentified
 18-NOV-2004
 02-SEP-2004.
 Turkson J,
 ADR40509;
 Query Match
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Gaps

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The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF sequence) cell-penetrating polypeptide of the invention.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 127.
 Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 Score 47; DB 8; Length 21; Pred. No. 0.98;
 0; Mismatches
 Disclosure; Page 219; 626pp; English.
 Borrello MA;
 ADK50915 standard; peptide; 21 AA.
 61.8%;
91.7%;
 10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
 10-JUN-2003; 2003WO-US018252.
 10-JUN-2002; 2002US-0386738P.
 11-DEC-2002; 2002US-0432241P. 23-APR-2003; 2003US-0464650P.
 10-JUN-2003; 2003WO-US018252.
 04-NOV-2004 (first entry)
 11; Conservative
 AVAAVLLPVLLA 19
 6 AAAAVLLPVLLA 17
 Zauderer M, Evans EE,
 (VACC-) VACCINEX INC. (UYRP) UNIV ROCHESTER.
 (VACC-) VACCINEX INC
 WPI; 2004-062349/06.
 Local Similarity
 WO2003104428-A2.
 WO2003104428-A2
 Sequence 21 AA;
 Unidentified
 Homo sapiens
 18-DEC-2003.
 18-DEC-2003.
 ADK50915;
 Query Match
 Matches
 RESULT 35
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 The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Raposi PGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 123.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 107.
 Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 0; Gaps
 C35 epitope, cytostatic, vaccine, tumour; breast, bladder carcinoma, human, Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 C35 epitope, cytostatic, vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 61.8%; Score 47; DB 8; Length 21; 100.0%; Pred. No. 0.98; o; Indels :ive 0; Mismatches 0; Indels
 Disclosure; Page 223; 626pp; English.
 Borrello MA;
 ADK50895 standard; peptide; 21 AA.
 10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
 10-JUN-2003; 2003WO-US018252
 04-NOV-2004 (first entry)
 04-NOV-2004 (first entry)
 Local Similarity 100.
 7 AAAVLLPVLLA 17
 Zauderer M, Evans EE,
 (VACC-) VACCINEX INC. (UYRP) UNIV ROCHESTER
 WPI; 2004-062349/06
 WO2003104428-A2
 Sequence 21 AA;
 Homo sapiens.
Unidentified.
 Homo sapiens
Unidentified
 18-DEC-2003
 ADK50895;
ADK50911;
 Query Match
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Matches

8 g RESULT 38 ADK50895

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Gape

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WPI; 2004-062349/06.
 Local Similarity
 WO2003104428-A2.
 Sequence 21 AA;
 Sequence 22 AA;
 04-NOV-2004
 Unidentified
 Homo sapiens
 18-DEC-2003
 ADK50923;
 Query Match
 Matches
 RESULT 41
 ADK50923
8888888888888
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 The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 111.
 Gaps
 C35 epitope, cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 The invention relates to a novel isolated polypeptide comprising or
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0
 61.8%; Score 47; DB 8; Length 21; 100.0%; Pred. No. 0.98;
 0; Indels
 0; Mismatches
 Disclosure; Page 220; 626pp; English.
 Disclosure; Page 224; 626pp; English.
 Borrello MA;
 Borrello MA;
 ADK50899 standard; peptide; 21 AA.
 100.08;
 10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
 10-JUN-2003; 2003WO-US018252
 (first entry)
 Best Local Similarity 100.
Matches 11; Conservative
 9 AAAVLLPVLLA 19
 7 AAAVLLPVLLA 17
 Evans EE,
 (VACC-) VACCINEX INC. (UYRP) UNIV ROCHESTER.
(UYRP) UNIV ROCHESTER
 Zauderer M, Evans EE,
 NPI; 2004-062349/06.
 WPI; 2004-062349/06.
 WO2003104428-A2.
 Sequence 21 AA;
 Zauderer M,
 Homo sapiens
Unidentified
 04-NOV-2004
 18-DEC-2003
 ADK50899;
 Query Match
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consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
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 The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates qytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi PGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 135.
 Gaps
 C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 ö
 61.8%; Score 47; DB 8; Length 21; 91.7%; Pred. No. 0.98; ive 0; Mismatches 1; Indels
 Disclosure; Page 226; 626pp; English.
 Borrello MA;
 ADK50923 standard; peptide; 22 AA.
 10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
 10-JUN-2003; 2003WO-US018252.
 (first entry)
 11; Conservative
 8 AVAAVLLPVLLA 19
 6 AAAAVLLPVLLA 17
 (VACC-) VACCINEX INC. (UYRP) UNIV ROCHESTER.
 Zauderer M, Evans EE,
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the nuclear localisation domain of fibroblast growth factor flanked by the nuclear localisation domain of fibroblast growth factor flanked by the nuclear localisation signal (NLS) from the HIV-1 matrix protein. The immunosuppressive activity of this peptide was compared with that of the cytopher compared with that of the sydomEm polypeptide causes of the SydomEm polypeptide causes of the SydomEm polypeptide causes of the SydomEm polypeptide are equally effective. The SydomEm polypeptide exemplifies the complast translocation inhibitor polypeptide of the invention. Nuclear translocation inhibitor polypeptide through the cytoplasmic membrane control capable of delivering the polypeptide through the cytoplasmic membrane into a cell, and at least 2 nuclear translocation of certain cellular protein. In addition, since the nuclear translocation of certain cellular complypeptides can be used to inhibit nuclear translocation of certain cellular complypeptide inhibitors are useful as immunosuppression agents. The polypeptides can therefore be used for the treatment of immune diseases. The polypeptides can also be used for treating physical symptoms manifested by responses to allergens which can intitate a state of hypersensitivity, for the treatment of sepsis and in the prevention of septic shock, antiviral agents, tumour growth culturar genes
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 Nuclear translocation inhibitor polypeptides - comprising signal sequence for delivery through the cytoplasmic membrane and at least 2 nuclear
 The present sequence represents the HIV-IMEM polypeptide, which comprises
 SV40NEW polypeptide; signal peptide; fibroblast growth factor; 3400 large antigen; nuclear localisation signal; NLS; ambages antigen; nuclear localisation signal; NLS; simmunosuppressive activity; inhibition; nuclear translocation inhibitor; kappa immunoglobulin light chain expression; S. typhosa LPS; nuclear translocation; treatment; immune disorder; autoimmune disease; hypersenstivity; sepsis; prevention; septic shock; antiviral agent; tumour growth suppressor; HIV-IMEM.
 Gaps
 HIV-IMEM polypeptide used to inhibit kappa-Ig light chain expression.
 ö
Score 47; DB 8; Length 22; Pred. No. 1; Nismatches 1; Indels
 Nadler SG, Cleaveland JS, Blake J, Haffar OK;
 AAW56392 standard; peptide; 26 AA.
 Example 1; Page 29; 69pp; English.
 -
0
 (BRIM) BRISTOL-MYERS SQUIBB CO.
 97WO-US016217
 96US-0026978P.
97US-00928958.
61.8%;
 91.7%;
 05-AUG-1998 (first entry)
 11; Conservative
 6 AAAAVLLPVLLA 17
 AVAAVLLPVLLA 20
 localisation sequences.
 WPI; 1998-217028/19.
 Local Similarity
 WO9811907-A1.
 15-SEP-1997;
 20-SEP-1996;
12-SEP-1997;
 26-MAR-1998
 Synthetic.
 AAW56392;
 Query Match
 Matches
 RESULT 42
 AAW56392
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 (I) (polypeptide inhibitor of a cellular protein nuclear translocation) which comprises a signal sequence peptide capable of delivering (I) through a cytoplasmic membrane into the cell; and a nuclear localization signal sequence (NLS) present along with an immunosuppressant. (I) or its derivatives provide useful tools for introducing an exogenous polypeptide comprising an NLS into an intact cell to inhibit nuclear translocation of a cellular protein, for studying the role of nuclear translocation in the regulation of cellular processes. See AAY55812 for detailed uses of (I) and compositions contianing (I): The present sequence regulates a HIV-IMEM polypeptide fragment comprising the membrane translocation domain of fibroblast growth factor flanked by NLS from HIV-I matrix protein
 Cellular protein; nuclear translocation; nuclear localization signal; immunosuppressant; immune response; viral infection; immune disorder; rheumatosid arthritis; multiple sclerosis; juvenile-onset diabetes; NLS; systemic luque erytematosus; SLE; asthma; sepsis; tumor growth, HIV;
 The invention provides a composition comprising an isolated polypeptide
 Novel composition comprising a nuclear localization signal and an inhibitor of nuclear translocation, useful for preventing transplanted
 Gaps
 Gaps
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 Length 26;
 61.8%; Score 47; DB 3; Length 26; 70.6%; Pred. No. 1.2; rive 1; Mismatches 4; Indels
 4; Indels
 4.
 5
 Score 47; DB
Pred. No. 1.2;
 1; Mismatches
 systemic lupus erytematosus; SLE; asthma.
fibroblast growth factor; matrix protein
 Example 1; Page 26; 68pp; English.
 AAY55813 standard; peptide; 26 AA.
 (BRIM) BRISTOL-MYERS SQUIBB CO.
 Human immunodeficiency virus 1.
 HIV-IMEM polypeptide fragment.
 17
 98US-00072429.
 1 KKKRKAAAAVLLPVLLA 17
 61.8%;
 99WO-US008984
 1 KKKRKAAAAVLLPVLLA
 organ or tissue rejection.
 (first entry)
 Query Match
Best Local Similarity 70.6
Matches 12; Conservative
 12; Conservative
 WPI; 2000-062141/05
 Local Similarity
 Sequence 26 AA;
 Sequence 26 AA;
 06-MAR-2000
 26-APR-1999;
 04-MAY-1998;
 WO9957138-A1
 11-NOV-1999.
 Synthetic.
 Nadler SG;
 AAY55813;
 Query Match
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KKKYKAAVALLPAVLLA 17

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The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi PGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 128.
 Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 Score 47; DB 8; Length 33;
Pred. No. 1.6;
0; Mismatches 1; Indels
 Disclosure; Page 197; 626pp; English.
 Borrello MA;
 ADK50916 standard; peptide; 33 AA.
 10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
 10-JUN-2003; 2003WO-US018252.
 10-JUN-2003; 2003WO-US018252.
 (first entry)
 Local Similarity 91.7
 6 AAAAVLLPVLLA 17
 20 AVAAVLLPVLLA 31
 (VACC-) VACCINEX INC. (UYRP) UNIV ROCHESTER.
 Zauderer M, Evans EE,
 WPI; 2004-062349/06.
 WO2003104428-A2.
 WO2003104428-A2.
 Sequence 33 AA;
 Unidentified
 04-NOV-2004
 Homo sapiens
Unidentified
 Homo sapiens
 18-DEC-2003.
 18-DEC-2003
 ADK50916;
 Query Match
 Matches
 ADK50916
 RESULT
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 The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibzoblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 112.
 Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 20.
 Gaps
 carcinoma;
 C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcino human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 ö
 Length 33;
 1; Indels
 Match 61.8%; Score 47; DB 8; Local Similarity 91.7%; Pred. No. 1.6; es 11; Conservative 0; Mismatches 1
 Disclosure; Page 220; 626pp; English.
 Borrello MA;
 ADK50808 standard; peptide; 33 AA.
 ADK50900 standard; peptide; 33 AA.
 10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
 10-JUN-2003; 2003WO-US018252
 (first entry)
 (first entry)
 6 AAAAVLLPVLLA 17
 20 ávaávilévila 31
 (VACC-) VACCINEX INC. (UYRP) UNIV ROCHESTER.
 Zauderer M, Evans EE,
 WPI; 2004-062349/06.
 WO2003104428-A2
 Sequence 33 AA;
 Homo sapiens.
Unidentified
 04-NOV-2004
 18-DEC-2003.
 04-NOV-2004
 ADK50900;
 ADK50808;
 Query Match
 Matches
 RESULT 45
 ADK50900
 ADK50808
 SO CCC CCC CCC X S X L L L X L X L X L X L X L X X X L X X L X X L X X L X X L X X L X X L X X X L X X L X X L X X
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Gaps

Gaps

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The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoms, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 124.
Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
 Score 47; DB 8; Length 33;
Pred. No. 1.6;
0; Mismatches 1; Indels
 Disclosure; Page 219; 626pp; English.
 Disclosure; Page 223; 626pp; English.
 Borrello MA;
 ADK50912 standard; peptide; 33 AA.
 10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
 61.8%;
91.7%;
 10-JUN-2003; 2003WO-US018252.
 04-NOV-2004 (first entry)
 11; Conservative
 6 AAAAVLLPVLLA 17
 20 AVAAVLLPVLLA 31
 (VACC-) VACCINEX INC. (UYRP) UNIV ROCHESTER.
 Zauderer M, Evans EE,
 WPI; 2004-062349/06.
 Best Local Similarity
 WO2003104428-A2
 Sequence 33 AA;
 Homo sapiens.
Unidentified.
 18-DEC-2003.
 ADK50912;
 Query Match
 Matches
 RESULT 48
ADKS0912
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 The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 108.
 Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
 Gaps
 C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
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 0; Indels
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 Disclosure, Page 224; 626pp; English
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11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
 10-JUN-2002; 2002US-0386738P.
11-DEC-2002; 2002US-043224IP.
23-APR-2003; 2003US-0464650P.
 10-JUN-2003; 2003WO-US018252
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 (VACC-) VACCINEX INC. (UYRP) UNIV ROCHESTER
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 WPI; 2004-062349/06
 WO2003104428-A2
 Sequence 33 AA;
 Unidentified.
 Homo sapiens
 Zauderer M,
 Zauderer M,
 04-NOV-2004
 18-DEC-2003
 ADK50896;
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(first entry)

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Nuclear translocation inhibitor polypeptides - comprising signal sequence for delivery through the cytoplasmic membrane and at least 2 nuclear localisation sequences.
 Signal peptide; nuclear localisation signal; NLS; immunosuppressive activity; inhibition; nuclear translocation inhibitor; nuclear translocation; treatment; immune disorder; autoimmune disease; hypersensitivity; sepsis; prevention; septic shock; antiviral agent; tumour growth suppressor.
 Nuclear translocation inhibitor polypeptide of the invention.
 AAW56414 standard; peptide; 29 AA
 Claim 14; Page 45; 69pp; English.
 (BRIM) BRISTOL-MYERS SQUIBB CO.
21 AVAAVLLPVLLA 32
 WPI; 1998-217028/19.
 05-AUG-1998
 Unidentified
 WO9811907-A1
 15-SEP-1997;
 20-SEP-1996;
 12-SEP-1997;
 26-MAR-1998
 Nadler SG,
 AAW56414;
 Query Match
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 The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 136.
 Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
carcinoma. The current sequence is that of human C35 / Kaposi FGF (fibroblast growth factor) signal sequence MST (membrane-translocating sequence) cell-penetrating polypeptide of the invention.
 Gaps
 C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma; human; Kaposi FGF signal sequence h region MST; cell-penetrating; fibroblast growth factor; membrane-translocating signal.
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 ch 61.8%; Score 47; DB 8; Length 34; l Similarity 91.7%; Pred. No. 1.6; ll; Conservative 0; Mismatches 1; Indels
 Length 33;
 0; Indels
 61.8%; Score 47; DB 8;
100.0%; Pred. No. 1.6;
ive 0; Mismatches
 Disclosure; Page 226; 626pp; English.
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 ADK50924 standard; peptide; 34 AA.
 11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
 10-JUN-2002; 2002US-0386738P.
 10-JUN-2003; 2003WO-US018252.
 (first entry)
 11; Conservative
 7 AAAVLLPVLLA 17
 21 AAAVLLPVLLA 31
 Zauderer M, Evans EE,
 (UYRP) UNIV ROCHESTER
 (VACC-) VACCINEX INC
 WPI; 2004-062349/06.
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Best Local Similarity
Matches 11; Conserv
 Best Local Similarity
 WO2003104428-A2
 Sequence 34 AA;
 Sequence 33 AA;
 Homo sapiens.
Unidentified
 04-NOV-2004
 18-DEC-2003
 ADK50924;
 Query Match
 Matches
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Haffar OK;

Cleaveland JS, Blake J,

96US-0026978P. 97US-00928958.

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The present sequence exemplifies the nuclear translocation inhibitor polypeptide of the invention. Nuclear translocation inhibitor polypeptides comprise a signal sequence peptide capable of delivering the polypeptides comprise a signal sequence peptide capable of delivering the polypeptide through the cytoplasmic membrane into a cell, and at least 2 nuclear localisation signals (NLSs). The polypeptides can be used to inhibit nuclear translocation of a cellular protein. In addition, since the nuclear translocation of a cellular peptides can be used to the nuclear translocation of certain cellular peptides is required for the nuclear translocation of certain cellular polypeptides inhibitors are useful as immunosuppression agents. The polypeptides can therefore be used for the treatment of immune discrets including autoimmune diseases. The polypeptides can also be used for treating physical symptoms manifested by responses to allergens which can initiate a state of hypersensitivity, for the treatment of sepsis and in the prevention of septic shock, antivixal agents, thenour growth suppressors, and for transcriptionally modulating the expression of cellular genes
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		RC STRAIN-NREL Y-1140;  RA Genoscope; RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.  RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.  BEBL; CR382126; CAG98406.1;  SQ SEQUENCE 420 AA; 47286 MW; 56B7A79313B4B452 CRC64;  Query Match  S9.2%; Score 45; DB 2; Length 420;  Best Local Similarity 52.9%; Pred; No. 47;  Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps  QY 1 KKKRAAAAVLLPVLLA 17  SD 66 RSKRKAASSTPVPVVLA 82  RESULT 2  Q7SBW3	DC O'SBW3 PRELIMINARY; PRT; 157 AA. AC O'SBW3. AC O'SBW3. AC O'SBW3. DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update) DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) DF predicted protein. DN Name=NCUO7045.1; CN Name=NCUO7045.1; CN Name=NCUO7045.1; CN NCBI_TAXID=5141; CN NCBI_TAXID=5141; CN NCBI_TAXID=5141; CN NCBI_TAXID=11; CN NCBI_TAXID=11
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	888000000000000000000000000000000000000	719 720 720 722 722 722 723 726 729 730 733 734 734 735 735 735 735 735 735 735 735 735 735	

Jaranton J. Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Buller J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Schulte U., Schittennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kamyussells M., Maucell E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., cotina; Sordariomycetes; iaceae; Neurospora. nce update) ation update) 57 AA. ****

OCCK41 PRELIMINARY; PRT; 420 AA. OCCK41; 25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

RESULT 1 Q6CK41 ID Q6CK AC Q6CK DT 25-OC

ALIGNMENTS

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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M., Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahl B.B., Jin S.S., Koo H., Zismann V., Haiao J., Blunt S., Yanaken S.S., Vuterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
 Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M., Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B., Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 "In-depth view of structure, activity, and evolution of rice
 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative receptor-like protein kinase (Hypothetical protein
 Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC092389; AAM88626.1; -.
EMBL; AC113948; AAM84518.1; -.
EMBL; AE017114; AAPS4775.1; -.
 Buell R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 Buell R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
 41A650742C4C6144 CRC64;
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4; Mismatches 3;
 The Rice Chromosome 10 Sequencing Consortium;
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Hypotheriaal protein; Kinase; Receptor.
SEQUENCE 802 AA; 85525 MW; 41A650742C
 Created)
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InterPro, IPR000719; Prot kinase.
Pfam, PF00560; LRR 1, 9.
PRINTS; PR00019; LEURICHRPT.
 57.9%;
 Science 300:1566-1569(2003).
 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 05-JUL-2004 (TrEMBLrel. 27,
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 PRELIMINARY;
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 NCBI_TaxID=39947;
 OSJNBb0038A07.18)
 chromosome 10
 Q8L4U4;
Q8L4U4;
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 Query Match
 RESULT 4
Q8L4U4
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Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Pauleen I., Sachs M.S., Lander B.S., Nusbaum C., Birren B.; The Genome Sequence of the Filamentous Fungus Neurospora crassa."; Nature 0:0-0(2003).

-I- CAUTION: The sequence shown here is derived from an EMBL/Geneark, DDBJ whole genome shotgun (WGS) entry which is
 Oryza gativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
 GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005535; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR007067; Znf_GATA.
InterPro; IPR000679; Znf_GATA.
Ffam; PF00320; GATA; 1.
PROSITE; PS0011; AnP_GATA ZN FINGER 2; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2 1; UNKNOWN 1.
SEQUENCE 242 AA; 24923 MW; EFEZ95D0A8F8629E CRC64;
 ö
 ö
 Query Match 57.9%; Score 44; DB 2; Length 157; Best Local Similarity 64.3%; Pred. No. 28; Matches 9; Conservative 3; Mismatches 2; Indels
 57.9%; Score 44; DB 2; Length 242; 52.9%; Pred. No. 42;
 Indels
 . -.
C62F0E2DD3834F3B CRC64;
 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
P06712001.19 protein.
 4
 242 AA.
 4; Mismatches
 PRT;
 EMBL; AABX01000162; EAA33870.1;
SEQUENCE 157 AA; 17703 MW; C
 |::|:|||| : | ||
155 KEERRAAAAVAPTALA 171
 17
 126 RRERSAAPAVLLPV 139
 1 KKKRKAAAAVLLPV 14
 1 KKKRKAAAAVLLPVLLA
 Query Match 57.9
Best Local Similarity 52.9
Matches 9; Conservative
 PRELIMINARY;
 preliminary data.
 HSSP; P17679; 1GNF.
 Q8LR32; -.
 Name=P0671D01.19;
 NCBI_TaxID=39947;
 Gramene;
```

RESULT 3
CORLR32
ID GORRA
AC GORRA
DDT 01-0
DT 01-0
DT 01-0
DC 01-0
DC

08LR32; **Q8LR32** 

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Gaps

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3; Indels

Length 802,

ઠે 셤 582 AA

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Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
 GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
GO; GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:0006208; F:metalloendopeptidase activity; IEA.
InterPro; IPR000585; Hemopaxin.
InterPro; IPR000626; Peptidase_M.
InterPro; IPR000626; Pept_MIOA_MIZB.
InterPro; IPR000618; Pept_MIOA_MIZB.
InterPro; IPR000619; Pept_MIOA_MIZB.
Pfam; PF00045; Hemopaxin, 4.
Pfam; PF00045; Hemopaxin, 4.
Pfam; PF00045; Peptidase_MIO_N; 1.
 Borrell-Pages M., Arribas J.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF3106662; AG34676.2; -.
HSSP: P50281; 1BQQ.
MEROPS; M10.014; -.
 PROSITE; PS00546; CYSTEINE SWITCH; 1.
PROSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Metalloprotease; Protease.
SEQUENCE 582 As; 66068 MW; 390ECAA632D32DF8 CRC64;
 (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
 PRT;
 Matrix metalloprotease MT1-MMP.
 PRINTS; PRO0138; MATRIXIN.
SMART; SM00120; HX; 4.
SMART; SM00235; ZNMC; 1.
 513
 Query Match
Best Local Similarity 100.
 PRELIMINARY;
 PRELIMINARY;
 501 RPAATATLLPVLL
 7 AAAVLLPVLL 16
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10029;
 01-JUN-2001
01-JUN-2001
 01-OCT-2003
 Q6ND81;
 Q99PG1
 Q6ND81
 RESULT 6
Q99PG1
 RESULT 7
 QENDB1
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ô
 Phosphoserine intermediate (By similarity).

GPI-anchor amidated serine (Potential).

N-linked (GlCNAc. .) (Potential).
 cultures.";
Dev. Dyn. 204:48-56(1995).
-!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an alcohol + phosphate.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLUIAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
 Interprior in the phosphtse.

Pfam; PP00145; Alk phosphtse; 1.

PRINTS; PR00113; ALKPHPHTASE.

SWART; SM00098; alkPPc; 1.

PROSITE; PS00123; ALKALINE PHOSPHATASE; 1.

Glycoprotein; GPI-anchor; Hydrolase; Lipoprotein; Magnesium; Membrane; Multigene family; Phosphorylation; Signal; Zinc.

SIGNAL
 Alkaline phosphatase, tissue-nonspecific
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Gaps
 Crawford K., Weissig H., Binette F., Millan J.L., Goetinck P.F.; "Tissue-nonspecific alkaline phosphatase participates in the establishment and growth of feather germs in embryonic chick skin
 ISOZyme.
Removed in mature form (Potential).
 ö
 -!- SIMILARITY: Belongs to the alkaline phosphatase family.
 15-JUL-1999 (Rel. 38, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Alkaline phosphatase, tissue-nonspecific isozyme precursor (BC 3.1.3.1) (AP-TNAP) (Liver/bone/kidney isozyme).
 Query Match 56.6%; Score 43; DB 1; Length 519; Best Local Similarity 76.9%; Pred. No. 1.2e+02; Matches 10; Conservative 0; Mismatches 3; Indels
 519 AA.
 MEDLINE=96107571; PubMed=8563025;
 56760 MW;
 EMBL; U19108; AAA92562.1; -. HSSP; P05187; 1EW2.
 16
 :: :|||| :|||||
RRSPRAAAAAVLPVLL 17
 KKKRKAAAAVLLPVLL
 STANDARD;
 Gallus gallus (Chicken)
 519
 498
 109
 302 3
429 4
519 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9031;
 499
 109
 CHICK
 CARBOHYD
CARBOHYD
CARBOHYD
 CARBOHYD
CARBOHYD
SEQUENCE
 ACT_SITE
 PROPEP
 Gallus
 CHAIN
 LIPID
 RESULT 5
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ö STRAIN=CGANO9 / ATCC BAA-98;
PubMed=14704707; DOI=10.1038/nbt923;
Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
Harrison F.H., Gibson J., Harwood C.S.; Gape ö Rhodopseudomonas palustris. Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; 56.6%; Score 43; DB 2; Length 582; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein precursor.
OrderedLocusNames=RPA0228; Bradyrhizobiaceae; Rhodopseudomonas. NCBI_TaxID=1076; 

4 RKAAAAVLLPVLL 16

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EMBL;
EMBL;
EMBL;
EMBL;
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 STRAIN=C57BL/63; TISSUB=Kidney, Parthenogenote, and Tongue; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazadi Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 STRAIN=CS7BL/61; TISSUE=Kidhey, Parthenogenote, and Tongue;
The PANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
 01-UDN-2001 (TrEMBLrel. 17, Created)
01-UDN-2001 (TrEMBLrel. 17, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annocation update)
Mus.musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310039H17 product:hypothetical NUDIX hydrolase
containing protein, full insert sequence (Mus musculus adult male
kidney CDNA, RIKEN full-length enriched library, clone:0610012H14
product:hypothetical NUDIX hydrolase containing protein, full insert
sequence) (Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN
full-length enriched library, clone:B130046A04 product:hypothetical
NUDIX hydrolase containing protein, full insert sequence) (Nucleoside dibhosphate linked moiety X)-type motif 8).
 STRAIN=CS7BL/67; TISSUE=Kidney, Parthenogenote, and Tongue;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 Gaps
 Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
 "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
 ö
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney, Parthenogenote, and Tongue;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 2; Length 133;
"Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris."; Nat. Blotechnol. 22:55-51 (2004). EMBL, BX572593; CAR25672.1; Complete proteome, Hypothetical protein; Signal.
 STRAIN=C57BL/6J; TISSUE=Kidney, Parthenogenote, and Tong
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 133 AA; 14481 MW; E22F622199718B5B CRC64;
 Score 42; DB 2
Pred. No. 52;
1; Mismatches
 atch 55.3%;
cal Similarity 76.9%;
10; Conservative
 5 KAAAAVLLPVLLA 17
 |: || |||||||
12 KSTAARLLPVLLA 24
 PRELIMINARY;
 RIKEN FANTOM Consortium;
 musculus (Mouse)
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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 SEQUENCE FROM N.A.
 SEQUENCE
 SIGNAL
 Q9CR24
 RESULT 8
Q9CR24
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B. Shibate K. Itoh M., Aitswar K. Nagonote S., Sasahiro H., Itoh M., Aitswar K. Nagonote S., Sasahiro H., Itoh M., Aitswar K. Nagonote S., Sasahiro H., Itoh M., Aitswar M., Nahiro K., Kathurah T., Tashiro H., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Manacoto R., Matamoto H., Saguduth S., Logani T., Kashiyah K., Manacoto R., Matamoto H., Saguduth S., Logani T., Kashiyah K., Manacoto R., Matamoto R., Matamoto R., Manacoto R., Maramoto R., Maramoto R., Manacoto R., Maramoto R., Manacoto R., Maramoto R., Manacoto R., Maramoto R., Manacoto R., Manacoto R., Manacoto R., Manacoto R., Maramoto R., Manacoto R., Manaco
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Q72PH8

RESULT 9 Q72PH8

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SEQUENCE FROM N.A.

STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
STRAIN=5601 / Serogroup Icterohaemorrhagiae / Serovar lai;
A RED S.-X., FUG., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
A Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
A Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
A Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
A Yeo Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
A Xu J.-G., Zhao G.-F.,
Intique physiological and pathogenic features of Leptospira
Interrogans revealed by whole-genome sequencing.";
B MBLA ASZ. 1888-893 (2003).
B EMBLA ASZ. 1806-893 (2003).
 "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).
EMBI; AE014684; AAN244441.;
Interpro; IPR002725; DUF45.
Interpro; IPR006025; Pept_M_Zn_BS.
 STRAIN=NCC 2705;
MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
 Bacteria, Actinobacteria, Actinobacteridae, Bifidobacteriales;
Bifidobacteriaceae, Bifidobacterium.
 Score 42; DB 2; Length 221;
Pred. No. 83;
 Score 42; DB 2; Length 268;
Pred. No. 99;
 2; Indels
 Indels
 221 AA; 25241 MW; 9119A0A728BCE258 CRC64;
 29679 MW; 04F91A150C29085E CRC64;
 Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 55.3%; Scor.
53.3%; Pred. No. oc.
 293 AA
 Pfam, PF01863; DUF45; 1. PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 4; Mismatches
 Created)
 Created)
 PRT;
 160 ERKROAAAINAALPOLLA 178
 1 KKKRKAAAAV--LLPVLLA 17
 Query Match
Best Local Similarity 57.9%;
Matches 11; Conservative
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
 (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 24,
 | ||| |:|:|
25 KFRKAIVAILMPMIL 39
 01-MAR-2003 (TrEMBLrel. 23,
 2 KKRKAAAAVLLPVLL 16
 OrderedLocusNames=BL0621;
 Local Similarity 53.3
Les 8; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Bifidobacterium longum
 Hypothetical protein.
 Complete proteome. SEQUENCE 268 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=216816;
 Complete proteome
 01-MAR-2003 (
01-MAR-2003 (
01-JUN-2003 (
 SEQUENCE
 Query Match
 Q8FYJ9
Q8FYJ9;
 QBGGLB
 RESULT 11
Q8G6L8
 Matches
 RESULT 12
 OBFYJ9
 ACCOUNT TO THE PROPERTY OF T
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 Pubmed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
Pubmed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
Pubmed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B., A. Marques M.V., Ollveira M.C., Menck C.F.M., Leite L.C.C., Carrer H., Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H., A. Goutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H., Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R., A., Goldman G.H., Goldman M.H.S., Marino C.L., Nunes L.R., A. Joronimo S.M.B., Lemos B.G.M., Lemos M.V.P., Marino C.L., Nunes L.R., A. Gollveira R.C., Pereira G.G., Reis M.S., Schriefer A., Gamargo L.B.A., Kitajima J.P., Setubal J.C., Van Sluys M.A., Camargo L.B.A., Kitajima J.P., Setubal J.C., Van Sluys M.A., Thovel insights into physicalogy and pathogenesis.";

D. Backeriol. 186:2164-2172(2004).

R. Backeriol. 186:2164-2172(2004).
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 Gaps
 Gaps
 OrderedLocusNames=LA1202;
Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira
 Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
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 55.3%; Score 42; DB 2; Length 221; 53.3%; Pred. No. 83;
 DB 2; Length 210;
 Indels
 3; Indels
 Hydrolase, Hypothetical protein.
SEQUENCE 210 AA; 23253 MW; 2E153033C466A6FE CRC64;
 221 AA; 25241 MW; 9119A0A728BCE258 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 Last sequence update)
Last annotation update)
 221 AA.
 221 AA.
 4; Mismatches
 3; Mismatches
 80;
 55.3%; Score 42; 60.0%; Pred. No.
 MGD; MGI:1913637; Nudt8.
GO; GO:0005739; C:mitochondrion; IDA.
InterPro; IPR000086; NUDIX_hydrolase.
Pfam; PF00293; NUDIX; 1.
 Created)
 PRT;
 PRT;
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
 KKRKAAAAVLLPVLL 16
 2 KKRKAAAAVLLPVLL 16
 : | ||||||:|: |
26 RSRPAAAAVLVPLCL 40
 KFRKAIVAILMPMIL 39
 Putative lipoprotein.
OrderedLocusNames=LIC12493;
 9; Conservative
 8; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Hypothetical protein.
 Query Match
Best Local Similarity
Matches 9; Conserv
 Query Match
Best Local Similarity
 Complete proteome.
 SEQUENCE FROM N.A.
 NCBI_TaxID=44275;
 Copenhageni).
 SEQUENCE
 SEQUENCE
 Q8F6U9;
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Gaps

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QBF6U9

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Best Loc Matches

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Q8K012;
 Q8K0I2
 RESULT 15
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 MEDLINE-22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
MEDLINE-22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
MEDLINE-22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
MEAUSEN T.T., Sebhadri R., Melacho K.E., Brinkac L.M., Beanan M.J.,
Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
M. Andson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
M. Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
M. Salzberg S.E., Hoover D.L., Lindler L.B., Halling S.M., Boyle S.M.,
M. Tabe Brucella suis genome reveals fundamental similarities between
The Brucella suis genome reveals fundamental similarities between
The Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 SEQUENCE FROM N.A.

STRAIN=16M / ATCC 23456 / Biotype 1;

STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;

DelVecchio V.G., Kapatral N., Redkar R.J., Patra G., Mujer C., Los T.,

Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N.C., Overbeek R.;

"The genome sequence of the facultative intracellular pathogen

Brucella melitensis.";
 Gaps
 Gaps
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 Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
NCBI_TaxID=29461;
 Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
NCBI_TaxID=29459;
 55.3%; Score 42; DB 2; Length 293; 81.8%; Pred. No. 1.1e+02; ive 2; Mismatches 0; Indels
 55.3%; Score 42; DB 2; Length 297; 81.8%; Pred. No. 1.1e+02; ive 2; Mismatches 0; Indels
 293 AA; 30733 MW; 4DFD4347112050AE CRC64;
 297 AA; 31306 MW; E8CA2D3CEAB94B85 CRC64;
 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
TRANSPORTER, DME FAMILY.
OrderedLocusNames=BMEI0187;
 Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 297 AA
 PRT;
 GO; GO:0016020; C:membrane; IEA.
InterPro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 1.
 GO; GO:0016020; C:membrane; IEA.
Pfam; PF00892; DUF6; 1.
 AE009460; AAL51369.1; -.
 Membrane protein, putative.
OrderedLocusNames=BR1873;
 Query Match 55.3
Best Local Similarity 81.8
Matches 9; Conservative
 9; Conservative
 |||:||:||||
156 AAALLIPVLLA 166
 PRELIMINARY;
 7 AAAVLLPVLLA 17
 Brucella melitensis.
 Best Local Similarity
Matches 9; Conserv
 SEQUENCE FROM N.A.
 Complete proteome
SEQUENCE 293 AA
 Complete proteome
 Brucella suis.
 TIGR; BR1873;
 SEQUENCE
 Query Match
 Q8YJ99
 RESULT 13
(198799)
AC Q88799
DT O1-MA
DT O1-TO
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DE OTANNS
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RECOURDINGE FROM N.A.

SEQUENCE FROM N.A.

RECOURDING 2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA MIDENINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA AIBENINE R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA AIBENIN S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhar N.K.,

RA AIBENIN S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boask S.A., McEwan P.J., McKernan K.J., Malak V.J., Hulyk S.W.,

RA Normstein M.J., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

RA Paley J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madran A., Young A.C., Shevchenko Y., Boufferd G.G.,

Mhiting M., Marimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Nofiguez A.C., Grimmood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

""" "Generation and initial analysis of more than 15,000 full-length human
 ö
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 ö
 Query Match 55.3%; Score 42; DB 2; Length 524; Best Local Similarity 53.3%; Pred. No. 1.8e+02; Matches 8; Conservative 4; Mismatches 3; Indels
 STRAIN-mix FVB/N; TISSUE-Mammary tumor;
Straubacrg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0313868; AAH31368.1; -.
 524 AA; 59060 MW; 27A07F39195F2F0D CRC64;
 Last sequence update)
Last annotation update)
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 PROSITE; PS00063; ALDOKETO REDUCTASE 3; UNKNOWN 1. PROSITE; PS50005; TPR; 5. REDUCTASE 3; UNKNOWN 1. PROSITE; PS50293; TPR REGION; 1. Repeat; TPR repeat. SEQUENCE 524 AA; S9060 MW; 27A07F39195F2F0D CR
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InterPro; IPR001395; Aldo/ket_red.
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InterPro; IPR001440; TPR.
FEam, PF00515; TPR_1; 4.
 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
 220 KKKKPVAAIILGILL 234
 2 KKRKAAAAVLLPVLL 16
 8; Conservative
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160 AAALLIPVLLA 170
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 STANDARD;
7 AAAVLLPVLLA 17
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ID PTIB BACSU
AC P54715;
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 RA KUNDINES-80440431; PubMedes-9384377; DOI=10.1038/3768;
RA KUNBELNES-980440403; PubMedes-9384377; DOI=10.1038/3768;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Brunschi C.V., Caldwell B., Capuano V., Carter N.M.,
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RA Broizot F., Deviner K.M., Dusterhoft A., Erhilch S.D., Rammerson P.T.,
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RA Ginseppi G., Guy B.J., Hage K., Haichly B.J., Grandi G.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
A Guiseppi G., Guy B.J., Hage K., Haichly B.J., Rananta D., Kaamata Y., Klaerr-Blanchard M.,
A Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
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A Kunano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Mediua N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
Roback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Prescott A.M., Presecan E., Puincelle B., Rapoport G.,
RA Prescott A.M., Presecan E., Puincelle B., Rapoport G.,
RA Scoffone F., Sakiguchi J., Sakowska A., Seror S.J., Serror P.,
RA Scoffone F., Sakiguchi J., Sakowska A., Seror S.J., Serror P.,
RA Tognoni A., Togato V., Wohlyama S., Wandenbol M., Vannier F.,
Wattzenegger T., Winteres P., Wipat A., Yamamoto H., Yamane K.,
Wattzenegger T., Winteres P., Wipat A., Yamamoto H., Yamane K.,
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Wassunotti A., Viari A., Wambutt R., Wedler E., Wedler H., Yamane K.,
Whitheres P., Winteres P., Wipat A., Yamanotti N., Yanane K.,
Whitheres P., Wipat A., Yamaneone E., Weller B., Reapoport G., Wanikawa H., Danchin A.,
Whitheres P., Wipat A., Yashawa H., Danchin A.,
Whitheres P., Wipat A., Yoshikawa H., Danchin A.,
Whitheres P., Wipat A., Yoshikawa H., Danchin A.,
Whitheres P., Wipat A., Yoshikawa H., Panchine B., Solde B., Solde B., Solde B., Solde B., Solde B., So
 Bacteriol. 183:5110-5121(2001).
--- FUNCTION: This is a component of the phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active transport system. The IICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phospho-HPP); IIA transfers its
01-OCT-1996 (Rel. 34, Createu, 01-OCT-1996 (Rel. 34, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) PTS system, arbutin-like IIBC component (Phosphotransferase enzyme II,
 phosphoryl group to the IIB domain which finally transfers it to
 CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein histidine + sugar phosphare.
SUBCELLULAR LOCATION: Integral membrane protein (Probable).
INDUCTION: By maltose; repressed by glucose.
 DOI=10.1128/JB.183.17.5110-5121.2001;
Yamamoto H., Serizawa M., Thompson J., Sekiguchi J.;
Regulation of the glv operon in Bacillus subtilis: YfiA (GlvR) is a positive regulator of the operon that is repressed through CcpA and
 Yamamoto H., Uchiyama S., Fajar A.N., Ogasawara N., Sekiguchi J.; "Determination of a 12 kb nucleotide sequence around the 76 degrees region of the Bacillus aubtilis chromosome."; Microbiology 142:1417-1421(1996).
 Name=glvC; Synonyms=glv-2, glvCB; OrderedLocusNames=BSU08200; Bacillus subtilis.
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1423;
 MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
 MEDLINE=21382183; PubMed=11489864;
 MEDLINE=96262713; PubMed=8704981;
 Nature 390:249-256(1997).
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 the sugar
 STRAIN=168;
 STRAIN=168
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.sib.ch).
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 Gaps
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 12 days embryo embryonic body below diaphragm region
cDNA, RIKEN full-length enriched library, clone:3732404C04
product:hypothetical Aldo/keto reductase family containing protein,
 R Subtiliat; B011848; glvC.

R InterPro; IPR01096; Ptrans_EIB.

R InterPro; IPR010975; Ptrans_EIC.

R InterPro; IPR010975; PTS_IIB_Calpha.

InterPro; IPR004719; PTS_IIB_Calpha.

R InterPro; IPR004719; PTS_IIIC_glc.

R Pfam; PP00378; PTS_EIIB; 1.

R PrODOm; PD001476; Ptrans_EIB; 1.

R TIGRFAMS; TIGR00825; pts_Glc; 1.

R TIGRFAMS; TIGR01998; PTS-II-BC-glcB; 1.

R TIGRFAMS; TIGR01998; PTS-II-BC-nag; 1.

R TIGRFAMS; TIGR01998; PTS-II-BC-nag; 1.

R TIGRFAMS; TIGR01998; PTS-II-BC-nag; 1.

R PROSITE; PS010135; PTS_EIIB_CYS; 1.

R ROMDJete protecome; Phosphotransferase system; Sugar transport; Transferase; Transmembrane; Transport.
 full insett sequence.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mommalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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 Phosphocysteine (By similarity).
D708C38048D4D63C CRC64;
 Score 42; DB 1; Length 527; Pred. No. 1.8e+02; 4; Mismatches 4; Indels
 607 AA.
SIMILARITY: Contains 1 PTS BIIB domain. SIMILARITY: Contains 1 PTS BIIC domain.
 Pred. No. 1.86
4; Mismatches
 Potential.
Potential.
 Potential
 Potential
 Potential
 Potential
 Potential
 Potential
 Potential
 Potential
 Potential
 Potential
 58055 MW;
 300 KEKKKLVAGLLIPVTL 315
 EMBL; D50543; BAA09105.1; -.
EMBL; Z99108; CAB12649.1; -.
PIR; G69635; G69635.
 55.3%;
 1 KKKRKAAAAVLLPVLL 16
 8; Conservative
 PRELIMINARY;
 28
79
1113
1152
1153
220
220
224
44
236
402
402
 527 AA;
 Best Local Similarity
 376
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Indels

3.

Mismatches

4

8; Conservative

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RESULT 17
Q8C4D2
 Matches
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 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Embryonic body below diaphragm region;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
 STRAIN=C57BL/6J; TISSUE=Embryonic body below diaphragm region, MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazadi Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 Adachi J., Alzawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayateu N., Hirancto K., Hiraoka T., Hirazane T., Hayateu N., Hirancto K., Hiraoka T., Hirazane T., Katoh H., Kawai J., Kojima Y., Ttoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Numazaki R., Ohon M., Ohsato N., Okazaki Y., Satok R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sakai C., Sakai K., Sakazume N., Sano H., Takaku-Akahira S., Takeda Y., Tanaka T., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A.
STRAIN=C57BL/63; TISSUE=Embryonic body below diaphragm region;
MEDLINE=99279235; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 STRAIN-C57BL/63; TISSUE-Embryonic body below diaphragm region; MEDLINE-2050913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Saseki N., Carninci P., Konno H., Akiyama J., Nishi K., Yasama T., Tashiro H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Tkegami T., Rashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 region;
 STRAIN=C57BL/6J; TISSUE=Embryonic body below diaphragm region;
 Score 42; DB 2; Length 607; Pred. No. 2.1e+02;
 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J, TISSUE=Embryonic body below diaphragm re
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/350S5500;
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PROSITE; PS50005; TPR; 3.
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SEQUENCE 607 AA; 67678 MW; E9F241C7DFC9FDC4 CRC64;
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 InterPro; IPR001440; TPR.
InterPro; IPR008941; TPR-like.
 55.3%;
 RIKEN FANTOM Consortium;
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 SMART; SM00028; TPR; 3.
 Query Match
Best Local Similarity
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 SEQUENCE FROM N.A.
 SEQUENCE
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Ronno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watshiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RIKEN integrated sequence analysis (RISA) system-384-format

T. sequencing pipeline with 38# multicapillary sequencer.";
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MNB musculus 0 day neonate creebellum cDNA, RIKEN full-length enriched library, clone:C230059F03 product:hypothetical Aldo/keto reductase family containing protein, full insert sequence.
 The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
 MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nuramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 STRAIN=CS7BL/6J; TISSUE=Cerebellum; MEDLINE=59279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayaehizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
 STRAIN=C57BL/67; TISSUE=Cerebellum;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
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 437 KKKKPVAAIILGILL 451
 Nature 409:685-690(2001).
2 KKRKAAAAVLLPVLL
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 Name=4930403J22Rik;
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 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 08C4D2;
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01-MAR-2003
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Spinal cord;
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Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki A., Murata M., Obsato N., Okazoki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.
 Gaps
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 STRAIN=USDA110;
MEDLINE=22484998; PubMed=12597275;
Rancko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriquchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
 "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
BNA Ree: 9:189-197(2002).
BNBJ, AP005955; BAC50902.1; -.
GO; GO:0004381; F:guanylate cyclase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
InterPro; IPR007890; CHASE2.
InterPro; IPR001054; G:cyclase.
Pfam; PF05226; CHASE2; 1.
Pfam; PF05216; GHASE2; 1.
Pfam; PF0511; Guanylate_cyc; 1.
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 Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 55.3%; Score 42; DB 2; Length 621; 53.3%; Pred. No. 2.1e+02; ive 4; Mismatches 3; Indels
 Length 628;
 PEGM; PF00515; TPR 1, 4.
SWART; SM00028; TPR; 7.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS50005; TPR, REGION; 1.
PROSITE; PS50293; TPR REGION; 1.
Hypothetical protein; Repeat; TPR repeat.
SEQUENCE 621 AA; 69489 MW; 6B1BAD7319D2B1A6 CRC64;
 66669 MW; 162B19FB9DAA9342 CRC64;
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Last annotation update)
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 SMART; SM00044; CYC¢; 1.—
PROSITE; PS50125; GUANYLATE CYCLASES_2; 1.
Complete proteome; Lyase.
SEQUENCE 628 AA; 66669 MW; 162B19FB9DAA
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 MGD; MGI:1921050; 4930403J22Rik.
InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR008940; Prenyl_trans.
InterPro; IPR001440; TPR.
 Bradyrhizobiaceae; Bradyrhizobium.
 317 KKKKPVAAIILGILL 331
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 2 KKRKAAAAVLLPVLL 16
 (TrEMBLrel. 24,
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OrderedLocusNames=blr5637;
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Best Conservative
 Conservative
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 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=375;
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Matches
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Spinal cord; wEDALME2159; DOI=10.1101/gr.145100; wEDALME20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nokazaki Y., pubbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
 The PANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
 Spinal cord,
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 RIKEN FANTOM Consortium; "Punctional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 STRAIN=C57BL/6J;
TISSUE=Cerebellum, Diencephalon, Parthenogenote, Retina, and
 STRAIN=C57BL/6J;
TISSUE=Cerebellum, Diencephalon, Parthenogenote, Retina, and
 STRAIN=CS7BL/6J;
TISSUE=Cerebellum, Diencephalon, Parthenogenote, Retina, and
 IISSUE=Cerebellum, Diencephalon, Parthenogenote, Retina, and
 MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 741 AA.
 PRT;
 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
317 ALAAVLLPVLL 327
 PRELIMINARY;
 [5]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 STRAIN=C57BL/6J
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Nature 0:0-0(2003).
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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EMBL; AABX01000239; EAA32564.1; -..
GO; GO:0005622; C:intracellular; IEA.
GO; GO:000540; C:ribosome; IEA.
GO; GO:000541; P:protein biosynthesis; IEA.
InterPro; IPR00213; FiA.
InterPro; IPR002143; Ribosomal L1.
PROSITE: PSS0006; FHA. DOMAIN; I.
 Created)
 J. Cell Sci. 115:1635-1642(2002).
EMBL; AF404747; AAM12663.1; -.
EMSP; P32851; 1JTH.
INTERPRO; IPR010989; t-snare.
InterPro; IPR010727; T_SNARE.
 (TrEMBLrel. 21, C
(TrEMBLrel. 21, I
(TrEMBLrel. 25, I
 54.6%;
 1006 KKAKKAAAAALP 1018
 Local Similarity 40.79 tes 11; Conservative
 1 KKKRKAAAAVLLP 13
 9; Conservative
 PRELIMINARY;
 Hypothetical protein.
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=2788;
 01-JUN-2002
01-OCT-2003
 Syntaxin PM.
 01-JUN-2002
 SEQUENCE
 system.";
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 Query Match
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 Q8S4W4
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Q8S4W4
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 Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagoki T., Hiraoka T., Hirozane T., Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki A., Murata M., Nakamura M., Salich H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 Gaps
 MEDLINES.20330913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINES.20330913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yanjawke S., Inoue K., Togawa Y., Izawa M., Ohara B., Watsahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
sequencing pipeline with 384 multicapillary sequencer.";
 Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 ö
 Neurospora crassa.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 STRAIN=C57BL/6J;
TISSUE=Cerebellum, Diencephalon, Parthenogenote, Retina, and
 TISSUE=Cerebellum, Diencephalon, Parthenogenote, Retina, and
 55.3%; Score 42; DB 2; Length 741; 53.3%; Pred. No. 2.5e+02; ive 4; Mismatches 3; Indels
 PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS500293; TPR. FEGION; 1.
Hypothetical protein; Repeat; TPR repeat.
SEQUENCE 741 AA; 82962 MW; DID3A380DFA04A7F CRC64;
 Last sequence update)
Last annotation update)
 PRT; 1049 AA.
 Created)
 InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR008940; Prenyl_trans.
InterPro; IPR001440; TPR.
 ; AK045271; BAC32288.1; -. MGI:1921050; 4930403J22Rik
 AK043293; BAC31518.1; -. AK044391; BAC31900.1; -. AK049748; BAC33902.1; -.
 ||:| ||:| 437 KKKKPVAAIILGILL 451
 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein.
 2 KKRKAAAAVLLPVLL 16
 Best Local Similarity 53.3
Matches 8; Conservative
 PRELIMINARY;
 Pfam; PF00515; TPR 1; 4.
SMART; SM00028; TPR; 7.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A. STRAIN=OR74A;
 NCBI_TaxID=5141;
 Spinal cord;
 Query Match
 Q7S899;
 078899
 EMBL;
 EMBL;
 EMBL;
 RESULT 20
Q7S899
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 Porphyra yezoensis.
Eukaryota<u>;</u> Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 MEDLINE-21947832; PubMed=11950882; Dacks J.B., Doolittle W.F.; "Novel syntaxin gene sequences from Giardia, Trypanosoma and algae: implications for the ancient evolution of the eukaryotic endomembrane
 Gaps
 Gaps
 11,
 ö
 Length 346;
 55.3%; Score 42; DB 2; Length 1049; 69.2%; Pred. No. 3.5e+02; ive 1; Mismatches 3; Indels
 IndelB
1049 AA; 115605 MW; 144750ECE6A3D828 CRC64;
 Pfam; PF05739; SNARE; T. SWARE; T. SWARE; SWARE; SMARE; SSAGUSTE; PS50192; T. SNARE; 1. SEQUENCE 346 AA, 36283 MW; F729BF6E8F9F6F5B CRC64;
 Last sequence update)
Last annotation update)
 Score 41.5; DB 2;
Pred. No. 1.5e+02;
3; Mismatches 2;
 PRT; 346 AA.
 261 KKKRKKICCVVILVIAIIAAILIPVLI 287
 1 KKKRK------16
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Hypothetical protein.
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 Q6AYH8;
 Q6AYH8
 RESULT 24
Q6AYH8
 Matches
a
 ID ACC DDT TO DD
 ö
 Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
A Baldarelli R., Hill D.P. Bult C., Hume D.A., Guackenbush J.,
A Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Borhiml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
A Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
A Graserland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
A Grimmond S., Gustincich S., Hirokwa N., Jackson I.J., Jarvis B.D.,
A Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Maglott D.K., Maltais L., Marchionni L., McKenzie L., Miki H.,
A Nagashima T., Numata K., Okido T., Pertea G., Pesole G.,
A Petrovsky N., Fillai R., Pontius J.U., Qi D., Ramachandran S.,
 STRAIN=BALB/C; TISSUB=Uterus; Ulrich R., Gerhauser I., Seeliger F., Baumgaertner W., Alldinger S.; Ulrich R., Gerhauser I., Seeliger F., Baumgaertner W., Alldinger S.; "Expression profile of matrix-metalloproteinases and their inhibitors in actue and chronic demyelinating Theiler's murine
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 ö
 STRAIN=C57BL/6J; TISSUE=Teetis;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 Length 67;
 STRAIN=BALB/c; TISSUE-Uterus;
Ulrich R.G., Seeliger F., Alldinger S., Baumgaertner W.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
 0; Indels
 52CDDDF3957E3FBA CRC64;
 Last sequence update)
Last annotation update)
 DB 2;
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hypothetical UPF0193 protein EVG1 homolog.
Mus musculus (Mouse).
 67 AA.
 Mismatches
 Score 41; DB
Pred. No. 41;
 Matrix metalloproteinase 14 (Fragment).
 Created)
 encephalomyelitis.";
Acta Neuropathol. 108:366-366(2004)
 67 AA; 7104 MW;
 53.9%;
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 EMBL; AY622974; AAT46405.1;
 Query Match
Best Local Similarity 81.0.
Post Local 9; Conservative
 STANDARD;
 6 AAAAVLLPVLL 16
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 63
 Name=Mmp14;
 EVG1 MOUSE
 SEQUENCE
 Q6GX97
 EVG1_MOUSE
 RESULT 22
 26GX97
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 RAY Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Atlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Atlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Expleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., Usdin T.B., Toohhyuki S., Carninci P., Prange C.,
RA Richards S., Worley K.C., Males S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.M., Sodergren B.J., Lu X., Ginbbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RXzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 ö
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sandelin R., Takenaka Y., Taylor M.S., Tasadale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney B., Hayashizaki Y., Ihm mouse based on functional annotation of
 Rāttus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Rattus.
 Gaps
 ö
 Length 216;
 2; Indels
 216 AA; 24737 MW; 5A36D524DC7AEF6B CRC64;
 60,770 full-length cDNAB.";
Nature 420:563-573(2002).
-!- SIMILARITY: Belongs to the UPF0193 (EVG1) family.
 Last sequence update)
Last annotation update)
 Score 41; DB 1; I
Pred. No. 1.2e+02;
 4; Mismatches
 Created)
 EMBL; AKO06539; BAB24642.1; -. MGD; MGI:1920774; 1700088E04Rik. InterPro; IPR007914; UPF0193.
 53.9%;
 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
 :|||:||:||:||
76 KKAASAIYLPPILA 89
 Pfam; PF05250; UPF0193; 1. Hypothetical protein. SEQUENCE 216 AA:
 4 RKAAAAVLLPVLLA 17
 8; Conservative
 PRELIMINARY;
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|||||: |::: |:||
157 KRKASIALIITVILA 171
 |:| || :| || ||
172 KKKKAAKILGPLLLA 186
 3 KRKAAAAVLLPVLLA 17
 3 KRKAAAAVLLPVLLA 17
 8; Conservative
 Best Local Similarity 60.0
Matches 9; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Thraustochytrium aureum.
Mitochondrion.
 Local Similarity
 SEQUENCE FROM N.A. STRAIN=PEST;
 Q7QB91;
01-MAR-2004
 Query Match
 Query Match
 AgCP2447
 Q7QB91
 056264
 RESULT 28
Q56264
ID Q5626
 RESULT 27
Q7QB91
 Matches
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fones S.J., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human
 MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
B Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
A Godie T., Goffeau A., Kahn D., Kise E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puthler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
R EMBL, AL591791; CAG4360.1; -
R GO; GO:0016021; C:integral to membrane; IEA.
R InterPro; IPR002781; DUF81: 1.
 Gaps
 Gaps
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 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL TRANSEMBRANE PROTEIN.
ORFNames=SMc03997;
Rhizobium meliloti (Sinorhizobium meliloti).
Raticobiaceaei Sinorhizobium/Ensifer group; Sinorhizobium.
 Score 41; DB 2; Length 216;
Pred. No. 1.2e+02;
4; Mismatches 2; Indels
 53.9%; Score 41; DB 2; Length 260; 72.7%; Pred. No. 1.4e+02;
 TISSUE-Testis;
Director MGC Project;
Director MGC Project;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC079039; AAH79039.1; -.
InterPro; IPR007914; UPF0193.
Pfam; PF05250; UPF0193; 1.
Hypothetical protein.
SEQUENCE 216 AA; 24648 MW; S045F48087D6DDDA CRC64;
 0; Indels
 Complete proteome; Hypothetical protein; Transmembrane. SEQUENCE 260 AA; 28137 MW; 8CFC59D49FF07A65 CRC64;
 Q9G4D8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome c oxidase subunit 3 (EC 1.9.3.1).
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 262 AA
 4; Mismatches
 3; Mismatches
 PRT;
 Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
 :|:|||: || :||
76 KKSAAAIYLPPILA 89
 4 RKAAAAVLLPVLLA 17
 PRELIMINARY;
 8; Conservative
 PRELIMINARY;
 |||:|||:||:
46 AAALLPILIA 56
 7 AAAVLLPVLLA 17
 Best Local Similarity
Matches 8; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE PROM N.A.
 NCBI_TaxID=382;
 and mouse
 Query Match
 Q92M69
 Q9G4D8
 Jones
 RESULT 26
Q9G4D8
 RESULT 25
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 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Subunits I, II and III form the functional core of the enzyme complex (By similarity).
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 C + 2 H(2)O.

-1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 3 family.

BMBL; AF288091; A623662.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:00162739; C:intochondrion; IEA.

GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.
 Gaps
 Gaps
 Anopheles gambiae str. PEST.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
 Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bukaryota; stramenopiles; Labyrinthulida; Thraustochytriidae;
Thraustochytrium.
NCBI_TaxID=42467;
 Length 262;
 Length 297;
 53.9%; Score 41; DB 2; Length 297
60.0%; Pred. No. 1.6e+02;
ive 3; Mismatches 3; Indels
 Preliminary data.
EMBL; AAAB01008880; EAA08668.1; -.
SEQUENCE 297 AA; 30551 MW; 7D60098FFE259BB5 CRC64;
 Mitochondrion; Oxidoreductase; Transmembrane.
SEQUENCE 262 AA; 29789 MW; C15163CF5C7EBCB8 CRC64;
 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 53.9%; Score 41; DB 2; I
53.3%; Pred. No. 1.4e+02;
iive 5; Mismatches 2;
 Name=agCG45893; ORFNames=ENSANGG0000017897;
 297 AA.
 342 AA
 InterPro; IPR000298; CytC_oxdse_III.
Pfam; PF00510; COX3; 1.
ProDom; PD000382; CytC_oxdse_III; 1.
PROSITE; PS50253; COX3; 1.
 PRT;
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
 "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";
 genomic sequence of nitrogen-fixing symbiotic bacterium
 MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.;
 Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Corynebacteriaceae, Corynebacterium.
 Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 53.9%; Score 41; DB 2; Length 403; 64.3%; Pred. No. 2.1e+02; artive 2; Mismatches 3; Indels
 403 AA; 43679 MW; 7FDD58F6F6A980AA CRC64;
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative transport protein.
OrderedLocusNames=CE1483;
 01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Genome Res. 13:1572-1579 (2003).

EMBL; AP005219; BAC18293.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.
 Bradyrhizobium japonicum USDA110.";
DNA Res. 9:198-197(2002).
EMBL; ASO05943; BAC47518.1; -.
InterPro; IPR001828; ANF_receptor.
Pfan; PP01094; ANF_receptor; 1.
Complete protecom.
 PRT;
 Bradyrhizobiaceae; Bradyrhizobium.
 | | |||::||:|:
151 KLKIAAAIILPLLV 164
 4 RKAAAAVLLPVLLA 17
 OrderedLocusNames=b112253;
 | ||| :|||:| |
8 RLAAACILLPMLAA 21
 Query Match
Best Local Similarity 64.3.
Best Local 9; Conservative
 Corynebacterium efficiens.
 PRELIMINARY;
 PRELIMINARY;
 InterPro; IPR007114; MFS
 SEQUENCE FROM N.A.
 NCBI_TaxID=152794;
 SEQUENCE FROM N.A.
 Bll2253 protein.
 NCBI_TaxID=375;
 STRAIN=YS-314;
 "Complete
 Q8FTS8;
 Q8FTS8
 RESULT 31
Q8FTS8
 RESULT 30
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 SEQUENCE FROM N.A.

STRAIN=ATCC 35405 / DSM 14222;
X PubMedia15064399; DOI=LO1073/pnas.0307639101;
A Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F., Bodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
A Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
Durkin S.A., Daugherty S.C., Sherty J., Shvartsbeyn A.,
A Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
A Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
Meinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
T "Comparison of the genome of the oral pathogen Treponema denticola
T with other spirochete genomes.";
Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
REMBL; AE017253; AASI2701.1; -.
 Gaps
 Gaps
 MEDLINE=95197228; PubMed=7534273; Ishihara K., Kuramitsu H.K.; "Cloning and expression of a neutral phosphatase gene from Treponema
 Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=158;
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 53.9%; Score 41; DB 2; Length 342; 57.1%; Pred. No. 1.8e+02; tive 4; Mismatches 2; Indels
 Query Match 53.9%; Score 41; DB 2; Length 346; Best Local Similarity 57.1%; Pred, No. 1.8e+02; Matches 8; Conservative 4; Mismatches 2; Indels
 NON TER 342 342
SEQUENCE 342 AA; 37951 MW; DAD677BE63073934 CRC64;
 346 AA; 38328 MW; 7CC63ECA7EA8D165 CRC64;
 Last sequence update)
Last annotation update)
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phosphatase (Fragment).
 PRT; 346 AA.
 denticola.";
Infect. Immun. 63:1147-1152(1995).
EMBL; L2421; AAA73940.1; -.
InterPro: IPR008934; AcDase_VanPerase.
InterPro; IPR0080326; Pesterase_PA_PTP.
Pfam; PP01569; PAP2; 1.
R SMART; SM0014; acidPPc; 1.
T NON_TER 342.
 InterPro; IPR008934; AcPase VanPerase.
InterPro; IPR000326; Pesterase PA_PTP.
 Created)
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, PAP2 family protein.
 Local Similarity 57.1%;
les 8; Conservative
 Pfam; PF01569; PAP2; 1.
SMART; SM00014; acidPPc; 1.
 | | |||::||:|:
151 KLKIAAAIILPLLV 164
 3 KRKAAAAVLLPVLL 16
 OrderedLocusNames=TDE2181;
 PRELIMINARY;
 Treponema denticola.
 SEQUENCE FROM N.A.
 Complete proteome.
 NCBI_TaxID=158;
 STRAIN=35405;
 Query Match
 073KN6;
 Q73KN6
 Best Loc
Matches
 RESULT 29
 Q73KN6
 ACCOOR SERVICE SERVICE
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Gaps

Khalak H.G.,

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NCBI_TaxID=279010;
 SEQUENCE FROM N.A.
 STRAIN=DSM 13;
PubMed=15383718;
 25-OCT-2004
25-OCT-2004
 Query Match
 Query Match
 Q62xr6
Q62xr6,
 065MC3
 Best Loc
Matches
 Matches
 RESULT 34
 RESULT 35
 Q65MC3
 Q62XR6
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 TISSUB=Frontal lobe left;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
Suzuki Y., Sugano S., Hashimoto K.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055261; BAB21885.1;
 Gaps
 Gaps
 SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
 Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini, Cercopithecidae;
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 Score 41; DB 2; Length 492;
Pred. No. 2.5e+02;
5; Mismatches 2; Indels
 53.9%; Score 41; DB 2; Length 524; 60.0%; Pred. No. 2.7e+02; ive 3; Mismatches 3; Indels
 PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS50093; TPR.REGION; 1.
Hypothetical protein; Repeat; TPR repeat.
SEQUENCE 524 AA; 59225 MW; 0ESESA95EEB0BB60 CRC64;
 492 AA; 50962 MW; 235E0CF3DA8EA1FF CRC64;
 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HP0486.
OrderedLocusNames=HP0486;
 524 AA.
 528 AA
 01-JAN-1998 (TrEMBLrel. 05, Created)
 PRT;
 PRT;
 Interpro; IPR001395; Aldo/Ket_red.
InterPro; IPR0018940; Prenyl_trans.
Interpro; IPR001440; TPR.
Pfam; PP00515; TPR 1; 5.
SMART; SM00028; TPR; 7.
 53.9%;
 ||:| |||:|
220 KKKKLIAAVVLGILL 234
 2 KKRKAAAAVLLPVLL 16
 4 RKAAAAVLLPVLLA 17
 ||| || ::|:::|
8 RKAPAAAIIPLMIA 21
 Cuery Match
Best Local Similarity 50.09
Matches 7; Conservative
PROSITE; PS50850; MFS; 1.
 PRELIMINARY;
 Local Similarity 60.0
 PRELIMINARY;
 Cercopithecinae, Macaca
 Complete proteome. SEQUENCE 492 AA;
 SEQUENCE FROM N.A.
 TaxID=9541;
 NCBI_TaxID=210;
 Query Match
Best Local S
Matches 9
 925E60
 025230
 RESULT 33
025230
 RESULT 32
 925860
SKB
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 TIGR; HP0486; -.

GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
Interpro; IFR003679; HP OMP 2.
Pfam; PF02521; HP OMP 2.
Complete proteome; Hypothetical protein.
SEQUENCE 528 AA; 59416 MW; ED37A2D668123430 CRC64;
 Gaps
 Gaps
Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weldman J.F., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
 an
 Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G.;
Ehrenreich A., Gottschalk G.;
"The Complete Genome Sequence of Bacillus licheniformis DSM13, Organism with Great Industrial Potential.";
J. MOL. Microbiol. Biotechnol. 7:204-211(2004).
EMBL, AE017333, AAUJ9791.1;
SEQUENCE 529 AA, 58301 MW; B05175B6038A0407 CRC64;
 ò
 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Phosphotransferase system (PTS) maltose-specific enzyme IICB
 Length 529;
 Length 528;
 53.9%; Score 41; DB 2; Length 528
61.1%; Pred. No. 2.7e+02;
ive 2; Mismatches 1; Indels
 4; Indels
 Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 component.
Name=malP; ORFNames=BL03019;
Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 53.9%; Score 41; DB 2; I
43.8%; Pred. No. 2.7e+02;
iive 5; Mismatches 4;
 529 AA
 530 AA
 PRT;
 (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last seq
(TrEMBLrel. 28, Last ann
 pylori.";
Nature 388:539-547(1997).
EMBL; AE000563; AAD07554.1; -.
PIR; F64580; F64580.
 2 KKRKAAAAVL----LPVL 15
 4 KKRKVAAALLKRFTLPLL 21
 Name=malP; ORFNames=BLi00857;
 |:|:| | :|:|
299 KEKKKIVAGLLIPITL 314
 16
 1 KKKRKAAAAVLLPVLL
 Local Similarity 61.1 nes 11; Conservative
 Local Similarity 43.8 tes 7; Conservative
 PRELIMINARY;
 PRELIMINARY;
 OS GREED DAY
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Hemopexin.

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InterPro; IPR000585;
 Name=MMP14;
 SITE
METAL
ACT SITE
 DOMAIN
TRANSMEM
DOMAIN
DOMAIN
 DISULFID
 SEQUENCE
 Query Match
 Zymogen.
 SIGNAL
 CHAIN
 MM14_HUMAN
 Matches
 RESULT 37
 셤
 ð
 MEDINE-9909592; PubMed=9881602; DOI=10.1016/S0945-053X(98)90098-1; MEDINE-9909592; PubMed=9881602; DOI=10.1016/S0945-053X(98)90098-1; Caron C., Xue J., Bartlett J.D.; Rembrane type 1 matrix Caron C., Xue J., Bartlett J.D.; Rembrane type 1 matrix metalloproteinase in tooth tissues."; Matrix Biol. 17:501-511(1998)...

Matrix Biol. 17:501-511(1998)...

Matrix Biol. 17:501-511(1998)...

LISUALIARARIY: Endopeptidase activity, May play a role in the biomineralization of enamel and dentin. Diomineralization of enamel and dentin.

LOTALIYITC ACTIVITY: Endopeptidase activity, Activates progelatinase A by cleavage of the propeptide at 37-Asn-|-Leu-38. Cher bonds hydrolyzed include 35-Gly-|-Ile-36 in the propeptide of collagenase 3, and 341-Asn-|-Phe-342, 441-Asp-|-Leu-442 and 34-Asn-|-The-355 in the aggreen interglobular domain.

LOGACTOR: Binds 1 zinc ion per subunit, calcium (By similarity).

LISSUE SPECIFICITY: Highly expressed in Geveloping tooth tissues.

LISSUE SPECIFICITY: Highly expressed in developing tooth tissues.

LISSUES SPECIFICITY: Highly expressed in developing tooth tissues.
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 ö
 "Complete genome sequence of the industrial bacterium Bacillus
licheniformis and comparisons with closely related Bacillus species.";
Genome Biol. 5:R77-R77(2004).
EMBL: CP000002; AAU22442.1; -.
 Gaps
 STRAIN=ATCC 14580;
Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J. Andra M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B. Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
 ö
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last amnotation update)
Martix metalloproteinase-14 precursor (EG 3.4.24.80) (MWP-14)
(Membrane-type matrix metalloproteinase 1) (MT-MMP 1) (MTWMP1)
(Membrane-type-1 matrix metalloproteinase) (MT-MWP) (MTNMP).
 53.9%; Score 41; DB 2; Length 530; 43.8%; Pred. No. 2.7e+02; tive 5; Mismatches 4; Indels
 530 AA; 58432 MW; B045829108BA0407 CRC64;
 580 AA.
 EMBL; AF067419; AAD38324.1; -. HSSP; P50281; 1BQQ.
MEROPS; M10.014; -.
 |:|:| | :|:|: |
KEKKKIVAGLLIPITL 315
 1 KKKRKAAAAVLLPVLL 16
 Local Similarity 43.8
les 7; Conservative
 STANDARD;
NCBI_TaxID=279010;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9823;
 Name=MMP14;
Sus scrofa (Pig)
 ransferase.
 MM14 PIG
Q9XT90;
 300
 SEQUENCE
 Query Match
 Best Loc
Matches
 RESULT 36
 MM14_PIG
MM1
 ò
 셤
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Gaps
 TISSUE=Placenta;
MEDLINE=95237627; PubMed=7721107; DOI=10.1016/0378-1119(94)00637-8;
Takino T., Sato H., Yamamoto E., Seiki M.;
"Cloning of a human gene potentially encoding a novel matrix
metalloproteinase having a C-terminal transmembrane domain.";
Gene 155:293-298(1995).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 PROSITE; PS00546; CYSTEINE SWITCH; 1.
PROSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Calcium; Hydrolase; Metalloprotease; Signal; Transmembrane; Zinc;
 'A matrix metalloproteinase expressed on the surface of invasive
 ö
 Zinc (catalytic) (By similarity). Zinc (catalytic) (By similarity).
 Cytoplasmic (Potential).
Cytoplasmic (Potential).
Hemopexin-like.
Cysteine switch (Potential).
Zinc (Catalytic) (By similarity).
By similarity).
 MEDLINE=94286011; PubMed=8015608; DOI=10.1038/370061a0;
Sato H., Takino T., Okada Y., Cao J., Shinagawa A., Yamamoto Seiki M.;
 Score 41; DB 1; Length 580;
Pred. No. 3e+02;
 Activation peptide.
Matrix metalloproteinase-14.
Extracellular (Potential).
 0; Indels
 B7B2C2C569A96CAC CRC64;
 2; Mismatches
 By similari
 Potential.
InterPro; IPR001818; Pept_M10A M12B.
InterPro; IPR006025; Pept_M Zn_BS.
InterPro; IPR006026; Pept_M Zn_BS.
Pfam; PF00045; Hemopexin; 4.
Pfam; PF00913; Peptidase_M10; 1.
Pfam; PF09393; Peptidase_M10, 1.
PRINTS; PR00138; MATRIXIN.
SMART; SM00120; HX; 4.
SMART; SM00235; ZnMc; 1.
 Potential
 65934 MW;
 53.9%;
 81.8%;
 9; Conservative
 :||||:|||||
536 SAAAVVLPVLL 546
 6 AAAAVLLPVLL 16
 Nature 370:61-65(1994).
 28
109
539
539
560
560
509
503
237
237
 Homo sapiens (Human)
 A;
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 TISSUE=Placenta;
 NCBI_TaxID=9606;
 1
29
1110
1110
5540
5561
314
237
 238
 tumour cells.";
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CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
 ACT SITE
METAL
 HELIX
TURN
SEQUENCE
 Query Match
 (MT-MMP)
 TURN
STRAND
TURN
HELIX
 MM14 MOUSE
11D MM14 MC
AC P516 MO
DT 16-0CT
DT 25-0CT
DE (Membri
D
 SITE
 Best Loc
Matches
 RESULT 38
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 Sato H., Kinoshita T., Takino T., Nakayama K., Seiki M.;

"Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP) by furin and its interaction with tissue inhibitor of metalloproteinases (TIMP) -2.";

FEBS Lett. 393:101-104(1996).

-!- FUNCTION: Seems to specifically activate progelatinase A. May thus trigger invasion by tumor cells by activating progelatinase A on the tumor cell surface.
-!- CATALYTIC ACTIVITY: Endopeptidase activity, Activates
SEQUENCE FROM N.A.
MEDLINE=95224014; PubMed=7708715;
Okada A., Bellocq J.P., Rouyer N., Chenard M.P., Rio M.C., Chambon P.,
 Stromal cells of human colon, breast, and head and neck carcinomas."; Proc. Natl. Acad. Sci. U.S.A. 92:2730-2734(1995).
 progelatinase A by cleavage of the properide at 37-Asn-|-Leu-38. Other bonds hydrolyzed include 35-Gly-|-Ile-36 in the propertide of collagenase 3, and 341-Asn-|-Phe-342, 441-Asp-|-Leu-442 and 354-Gln-|-Thr-355 in the aggreen interglobular domain. COPACTOR: Binds 1 zinc ion per subunit, calcium (By similarity). SUBCELLULAR LOCATION: Type I membrane protein (Potential). TISSUE SPECIFICITY: In stromal cells of colon, breast, and head
 "CDNA sequence and mRNA tissue distribution of a novel human matrix metalloproteinase with a potential transmembrane segment."; Eur. J. Blochem. 231:602-608(1995).
 [5]
SEQUENCE FROM N.A.
Luo G.X., Relsfeld R.A., Strongin A.Y.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
 Lohi J.L., Westermarck J., Kaehaeri V.M., Keski-Oja J.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
 SIMILARITY: Belongs to the peptidase M10A family. SIMILARITY: Contains 1 hemopexin-like domain.
 GO: GO: 0005887; C: integral to plasma membrane; TAS. GO; GO: 0005887; C: integral to plasma membrane; TAS. GO; GO: 000422; F: metalloendopeptidase activity; TAS. GO; GO: 0008270; F: zinc ion binding; TAS. GO; GO: 0006508; F: proteclysis and peptidolysis; TAS.
 InterPro; IPR000585; Hemopaxin.
InterPro; IPR001818; Pept MIOA MIZB.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR006026; Pept M Zn BS.
 TISSUE-Lung;
MEDLINE-95377289; PubMed-7649159;
Will H., Hinzmann B.;
 EWBL; D26512; BAA05519.1; --
EWBL; X83535; CAA58519.1; --
EWBL; X83535; CAA58519.1; --
EWBL; U41078; AAA83770.1; --
EWBL; X90925; CAA62432.1; --
FIR; I38028; I38028.
PDB; IBQQ; X-FAY; M=114-287.
PDB; LBUV; X-FAY; M=114-287.
 MEROPS; M10.014; -. Genew; HGNC:7160; MMP14.
 SEQUENCE OF 112-116.
 SEQUENCE FROM N.A.
 PubMed=8804434;
 and neck.
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 | PM14 | MOUSE | STANDARD; | PRT; | 582 AA. |
| PS1569; | O08645; | O35369; |
| O1-OCT-1996 (Rel. 34, Created) | 16-OCT-2001 (Rel. 40, Last sequence update) |
| S5-OCT-2004 (Rel. 45, Last annotation update) |
| Matrix metalloproteinase-14 precursor (EC 3.4.24.80) (MMP-14) |
| Membrane-type matrix metalloproteinase | MT-MMP | (MTMMP) |
| Membrane-type-1 matrix metalloproteinase) (MT1-MMP) (MTMMP) (MMP-XI)
 Gaps
 Cysteine switch (Potential).
Zinc (catalytic) (By similarity).
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
By similarity.
K -> B (in Ref. 2, 4, 5 and 6).
S -> P (in Ref. 6).
 ö
Pfam; PF00045; Hemopexin; 4.

Pfam; PF00413; Peptidase_M10; 1.

Pfam; PF004313; Peptidase_M10_N; 1.

PRINTS; PR00136; MATRIXIN.

SMART; SM00120; HX; 4.

SMART; SM00235; ZnMc; 1.

PROSITE; PS00546; CYSTEINE SWITCH; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

3D-structure; Calcium; Direct protein sequencing; Hydrolase;
 Length 582;
 Activation peptide.
Matrix metalloproteinase-14.
Extracellular (Potential).
 Indels
 Metalloprotease, Signal, Transmembrane, Zinc; Zymogen. SIGNAL 1 20 POtential. PROPEP 21 111 Activation peptide.
 65883 MW; EFCEDCE6A41116F9 CRC64;
 Potential.
Cytoplasmic (Potential).
 53.9%; Score 41; DB 1;
81.8%; Pred. No. 3e+02;
ive 2; Mismatches
 Hemopexin-like.
 Name=Mmp14; Synonyms=Mtmmp;
Mus musculus (Mouse).
 Conservative
 :||||:|||||
538 SAAAVVLPVLL 548
 6 AAAAVLLPVLL 16
 508
338
338
500
1128
1128
1135
1140
1170
 279 2
283 2
582 AA;
 Local Similarity
tes 9; Conserv
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or send an email to license@isb-sib.ch).
 EMBL; X83536; CAA58520.2; -.
EMBL; AF022432; AAB86602.1; -.
EMBL; AF022424; AAB86602.1; JUINED.
EMBL; AF022425; AAB86602.1; JUINED.
EMBL; AF022425; AAB86602.1; JUINED.
EMBL; AF022429; AAB86602.1; JUINED.
EMBL; AF022429; AAB86602.1; JUINED.
EMBL; AF022439; AAB86602.1; JUINED.
EMBL; AF022430; AAB86602.1; JUINED.
EMBL; AF022431; AAB86602.1; JUINED.
 InterPro; IPR000585; Hemopexin.
InterPro; IPR001818; Pept_MIOA_M12B.
InterPro; IPR006025; Pept M zn BS.
InterPro; IPR006026; PeptIdase_M.
 EMBL; U54984; AAB51753.1;
HSSP; P50281; 1BQQ.
 9; Conservative
 :||||:|||||
538 SAAAVVLPVLL 548
 6 AAAAVLLPVLL 16
 MGD; MGI:101900; Mmp14.
 582 AA;
 Local Similarity
 MEROPS; M10.014;
 CHAIN
DOMAIN
TRANSMEM
 ACT SITE
METĀL
 CONFLICT
CONFLICT
SEQUENCE
 CONFLICT
CONFLICT
CONFLICT
 CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
 Query Match
 DISULFID
 DOMAIN
 SITE
 Matches
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 STRAIN=129/Sv;
MEDLINE=946735; PubMed=9225265; DOI=10.1074/jbc.272.41.25511;
Apte S.S., Fukai N., Beier D.R., Olsen B.R.;
"The matrix metalloproteinase-14 (MMP-14) gene is structurally
distinct from other MMP genes and is co-expressed with the TIMP-2 gene
 Ota K., Stetler-Stevenson W.G., Yang Q., Kumar A., Wada J., Kashihara N., Wallner E.I., Kanwar Y.S., "Cloning of murine membrane-type-l-marrix metalloproteinase (MT-1-MMP) and its metanephric developmental regulation with respect to MMP-2 and
 SEQUENCE FROM N.A.
MEDLINE=95224014; PubMed=7708715;
Okada A., Bellocq J.P., Rouyer N., Chenard M.P., Rio M.C., Chambon P.,
 "Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells of human colon, breast, and head and neck carcinomas."; Proc. Natl. Acad. Sci. U.S.A. 92:2730-2734(1995).
 MEDLINE=99449306; PubMed=10520996; DOI=10.1016/S0092-8674(00)80064-1; HolDbock K., Blanco P., Caterina J., Yamada S., Kromer M., Kuznetsov S.A., Mankani M., Robey P.G., Poole A.R., Pidoux I., Ward J.M., Birkedal-Hansen H.; Ward J.M., Sirkedal-Hansen H.; Mard-Edicient mice develop dwarfism, osteopenia, arthritis, and connective tissue disease due to inadequate collagen turnover."; ell 99:81-92(1999).
 arteries, expressed at lower levels in the myocardium, cranicofacial mesenchyme, nasal epithelium and liver capsule. At days 14.5 and 17.5, expressed in the musculoskeltal system, an ossification areas, with continued expression in the arterial
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 -!- PTM: The precursor is cleaved by a furin endopeptidase (By
 Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
 -!- SIMILARITY: Belongs to the peptidase M10A family.
 during mouse embryogenesis.";
J. Biol. Chem. 272:25511-25517(1997).
 SEQUENCE FROM N.A.
STRAIN=CD-1; TISSUE=Kidney;
MEDLINE=98311877; PubMed=9648071;
 Kidney Int. 54:131-142(1998).
 SEQUENCE FROM N.A.
 media.
 NCBI_TaxID=10090;
 similarity).
 inhibitor
 tunica
 Basset P.;
 REVISIONS
 Odaka A.;
 FUNCTION.
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ö
 Gaps
R Pfan; PF0045; Hemopean; 4.

R Pfan; PF00413; Peptidase_M10; 1.

R Pfan; PF00413; Peptidase_M10; 1.

R PRINTS; PR001138; MATRIXIN.

R SMART; SM00120; HX; 4.

R SMART; SM00125; ZnMc; 1.

R PROSITE; PS00044; HEMOPEXIN; 1.

R PROSITE; PS00142; ZINC_PROTEASE; 1.

R PROPEP 21 111 By similarity.
 By similarity.

Zinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

By similarity.

P -> S (in Ref. 3).

A -> D (in Ref. 1).

S -> A (in Ref. 1).

N -> P (in Ref. 1).

K -> T (in Ref. 1).

FD -> CV (in Ref. 1).

PD -> CV (in Ref. 1).
 ö
 Cysteine switch (Potential).
Zinc (catalytic) (By similarity).
 53.9%; Score 41; DB 1; Length 582; 81.8%; Pred. No. 3e+02;
 Potential.

By similarity.

Matrix metalloproteinase-14.

Extracellular (Potential).
 Indels
 407 G -> V (in Ref. 1).

412 T -> S (in Ref. 1).

417 A -> T (in Ref. 1).

512 G -> R (in Ref. 4).

65935 MW; 3AB355158D4DD175 CRC64;
 Cytoplasmic (Potential).
 ;
0
 Hemopexin-like.
 582 AA.
 2; Mismatches
 RESULT 39
MM14 RABIT
ID — WM14 RABIT STANDARD;
1A — AAC Q95220; P79225;
DT 01-NOV-1997 (Rel. 35, Created)
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8444444448
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 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
 PRINTS; PRO0138; MATRIXIN. — SMART; SM00120; HX; 4.
SWART; SM00235; ZnMc; 1.
PROSITE; PS000546; CYSTEINE SWITCH; 1.
PROSITE; PS00142; HEMDEXIN; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
Calcium; Hydrolase; Metalloprotease; Signal; Transmembrane; Zinc;
 (By similarity).
 25-OCT-2004 (Rel. 45, Last annotation update)
Mattix metalloprotainase-14 precursor (EC 34.24.80) (MMP-14)
(Membrane-type matrix metalloprotainase 1) (MT-MMP 1) (MTMMP1)
(Membrane-type-1 matrix metalloproteinase) (MT1-MMP) (MTIMMP).
 (By similarity) (By similarity)
 Activation peptide.
Matrix metalloproteinase-14.
Extracellular (Potential).
Potential.
 Hemopexin-like.
Cysteine switch (Potential)
Zinc (catalytic) (By simila
By similarity.
 SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE=Vascular smooth muscle;
Wang H., Keiser J.;
 Wang H., Keiser J.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
 Cytoplasmic (Potential).
 Zinc (catalytic)
Zinc (catalytic)
 By similarity.
15-JUL-1998 (Rel. 36, Last sequence update)
 MERCES, MIC.014; -- ...
InterPro; IPRO00585; Pept_MIOA_MI2B.
InterPro; IPRO06025; Pept_MIOA_MI2B.
InterPro; IPRO06025; Pept_MIOA_MI2B.
InterPro; IPRO06025; PeptIdase_M.
Pfam; PF00045; Hemopexin; 4.
Pfam; PF000413; Peptidase_MI0; 1.
Pfam; PF00933; Peptidase_MI0, 1.
 (Rabbit)
 EMBL; U83918; AAB41500.1; -. EMBL; U73940; AAD13803.1; -.
 SEQUENCE OF 1-572 FROM N.A. STRAIN-New Zealand white;
 Oryctolagus cuniculus
 NCBI_TaxID=9986;
 METAL
DISULPID
 Zymogen.
SIGNAL
PROPEP
CHAIN
 DOMAIN
TRANSMEM
 Sato T.;
 DOMAIN
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 SEQUENCE FROM N.A.
MEDLINE=95224014; PubMed=7708715;
Okada A., Bellocg J.P., Rouyer N., Chenard M.P., Rio M.C., Chambon P.,
 "Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells of human colon, breast, and head and neck carcinomas.";
 Gapa
 Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
 (MT-
 ö
 01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Matrix metalloproteinase-14 precursor (EC 3.4.24.80) (WMP-14)
(Membrane-type matrix metalloproteinase 1) (WT-MMP 1) (MTMMP1)
(Membrane-type-1 matrix metalloproteinase) (WT1-MMP) (WT1MMP)
Q -> K (in Ref. 2).
K -> N (in Ref. 2).
L -> V (in Ref. 2).
E -> D (in Ref. 2).
RCLLN -> KYUPPP (in Ref. 2).
GQP -> RTT (in Ref. 2).
GLERIS -> RTPIPDK (in Ref. 2).
K -> N (in Ref. 2).
K -> N (in Ref. 2).
K -> L (in Ref. 2).
 Length 582;
 0; Indels
 F -> L (in Ref. 2).
L -> F (in Ref. 2).
844624BOAF1B6812 CRC64;
 stromal celis of human colon, breast, and head a Proc. Natl. Acad. Sci. U.S.A. 92:2730-2734(1995)
 Score 41; DB 1;
Pred. No. 3e+02;
 582 AA
 2; Mismatches
 MW.
 53.9%;
 EMBL; X83537; CAA58521.1; -. EMBL; X91785; CAA62897.1; -.
 81.8%;
 Name=Mmp14; Synonyms=Mtmmp;
 65963
 9; Conservative
 :||||:|||||
538 SAAAVVLPVLL 548
 STANDARD;
 6 AAAAVLLPVLL 16
 Best Local Similarity
Matches 9; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 RESULT 40
MM14 RAT
ID MM14 RAT
 CONFLICT
 Query Match
 CONFLICT
 Basset P
 010739
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53.9%;
81.8%;
 Query Match
Best Local Similarity 81.0%,
Best Local Sy Conservative
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538 SAAAVVLPVLL 548
 PRELIMINARY;
 6 AAAAVLLPVLL 16
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Caprinae; Capra.
NCBI_TaxID=9925;
 TISSUE-Placenta;
 TISSUE=Placenta;
 Name=MT1MMP
 Q9XSP0
Q9XSP0;
 RESULT 42
 09XSP0
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 Gaps
 Membrane-type matrix metalloprotesse 1.

Bos taurus (Bovins).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 PROSITE; PS00142; ZINC PROTEASE; 1.
Calcium; Hydrolase; Metalloprotease; Signal; Transmembrane; Zinc;
 Cytoplasmic (Potential).
Hemopexin-like.
Cysteine switch (Potential).
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
By similarity.
I -> M (in Ref. 2).
D -> A (in Ref. 2).
 A Zhang B., Yan L., Moses M.A., Fang J., Miao H., Tsang P.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AF2904291, AAG28170.1; -.
R EMBL, FSD281; 1BQQ.
R HSRP; FSD281; 1BQQ.
R MEROPS; M10.014; -.
R GO; GO:0004222; F:metalloendopptidase activity; IEA.
R GO; GO:0004222; F:metalloendopptidase activity; IEA.
R GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
R InterPro; IPRO06508; Peptidase M.
R InterPro; IPRO06508; Peptidase M.
R InterPro; IPRO06508; Peptidase M.
R InterPro; IPRO06025; Pept M10AM12B.
R InterPro; IPRO060070; PGBD_ITKe.
 ö
 Score 41; DB 1; Length 582;
Pred. No. 3e+02;
2; Mismatches 0; Indels
 Activation peptide.
Matrix metalloproteinase-14.
Extracellular (Potential).
 8B40FDD9999CA80C CRC64;
 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 582 AA.
 InterPro; IPR001819; Hemopexin.
InterPro; IPR001819; Pept_MIOA_MI2B.
InterPro; IPR001819; Pept_MIOA_MI2B.
InterPro; IPR006026; Pept_MICA_BS.
InterPro; IPR006026; Pept_MICA_BS.
InterPro; IPR006026; Pept_MICA_BS.
InterPro; IPR00613; Peptidase_MIO; 1.
Pfam; PF00413; Peptidase_MIO; 1.
PRNINTS; PR00139; MATRIXIN.
SWART; SW00213; ZMG; 1.
PROSITE; PS00546; CYSTEINE SWITCH; 1.
PROSITE; PS00546; CYSTEINE SWITCH; 1.
 66106 MW;
 53.9%;
 Query Match
Best Local Similarity 81.8,
 :||||:|||||
538 SAAAVVLPVLL 548
 PRELIMINARY;
 6 AAAAVLLPVLL 16
PIR; 184471; 184471.
HSSP; P50281; 1BQQ.
 582 AA;
 MEROPS; M10.014; -RGD; 620198; Mmp14
 SEQUENCE FROM N.A.
 NCBI_TaxID=9913;
 Bovinae; Bos
 Zymogen.
SIGNAL
PROPEP
CHAIN
DOMAIN
TRANSMEM
DOMAIN
 SITE
METAL
ACT SITE
METAL
 CONFLICT
CONFLICT
SEQUENCE
 DISULFID
 Q9GLE4
 RESULT 41
 Q9GLE4
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 MEDIJORE-1593431, PubMed=11757910;
MEDIJORE-1593432, PubMed=11757910;
Uekita T., Tanaka S.S., Sato H., Seiki M., Tojo H., Tachi C.;
"Expression of membrane-type 1 matrix metalloproteinase (MT1-MMP) in trophoblast and endometrial epithelial cell populations of the symppitheliochorial placenta of goats (Capra hircus).";
Arch. Histol. Cytol. 64:411-424(2001).
 TISSUEs-placenta;

Uckiata T., Tanaka S., Mariko Y., Sato H., Seiki M., Tojo H., Tachi C.;

Tachi C.;

Tachi C.;

Tachi C.;

Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB010921; BA36551.1; -.

R HSSP; P50281; 1BQD.

R RGOPS; M.O.014; -.

R GO, GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.

RO; GO:0005222; F:metalloendopeptidase activity; IEA.

RO; GO:000528; P:proteolysis and peptidolysis; IEA.

RICEPPO; IPR000585; Hemopexin.

R InterPro; IPR000585; Hemopexin.

R InterPro; IPR000585; Peptidase M.

RINTS; PR00138; Peptidase M.

R Pfam; PF00945; Hemopexin; 4.

R Pfam; PF00945; Hemopexin; 4.

R RNINTS; PR00138; MATRIXIN.

R SMART; SM00120; HX; 4.

R SMART; SM00120; HX; 4.

R ROSITE; PS00124; HEMOPEXIN; 1.

R ROSITE; PS00124; HEMOPEXIN; 1.
 Capra hirrus (Goat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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 Length 582;
 Length 582;
 Score 41; DB 2; Length 584
Pred. No. 3e+02;
 0; Indels
Pfam; PP00045; Hemopexin; 4.
Pfam; PP03933; Peptidase_M10_N; 1.
PRINTS; PR00138; MATRIXIN.
SWART; SW00120; HX;
SWART; SW00235; ZnMc; 1.
PROSITE; PS00044; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
MCABLIOPIOLEASE; PROTEASE.
SEQUENCE 582 AA; 65882 MW; 65174CE65D4040E1 CRC64;
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Membrane-type matrix metalloproteinase-1.
 Query Match 53.9%; Score 41; DB 2; Best Local Similarity 81.8%; Pred. No. 3e+02; Matches 9; Conservative 2; Mismatches
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01-MAR-2003
01-MAR-2003
 Name=Mmp14;
 OBBTX2
 Q8BTX2
 44
 ö
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 ;
0
 53.9%; Score 41; DB 2; Length 582; 81.8%; Pred. No. 3e+02;
 Indels
 Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
 PS00142; ZINC PROTEASE; UNKNOWN 1.
582 AA; 65931 MW; 28CFCE84FC0ACD1B CRC64;
 Last sequence update)
Last annotation update)
(Membrane-inserted).
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 ;
0
 582 AA.
 EMBL; BC076638; AAH76638.1; -. GO; GO:0005615; C:extracellular space; TAS. GO; GO:0016021; C:integral to membrane; TAS
 2; Mismatches
 PROSITE; PS00546; CYSTEINE SWITCH; 1. PROSITE; PS00024; HEMOPEXIN; 1.
 InterPro; IPR000585; Hemopexin.
InterPro; IPR006026; Peptidase M.
InterPro; IPR001818; Pept_M10A_M12B.
InterPro; IPR006025; Pept_M_Zn_BS.
 Created)
 Pfam; PF00045; Hemopexin; 4. Pfam; PF03933; Peptidase M10 N; 1. PRINTS; PR00138; MATRIXIN.
 SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Head;
 (TrEMBLrel. 28, (TrEMBLrel. 28, (TrEMBLrel. 28,
 Matrix metalloproteinase 14
 :||||:|||||
538 SAAAVVLPVLL 548
 PRELIMINARY;
 Conservative
 SMART; SM00120; HX; 4.
SMART; SM00235; ZnMc; 1.
6 AAAAVLLPVLL 16
 Mus musculus (Mouse)
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 5-0CT-2004
 <u>ه</u>
ن
 25-OCT-2004
 Name=Mmp14;
 PROSITE;
 SEQUENCE
 Query Match
 RESULT 43
Q6DFUS
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Matches
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:||||:|||| 538 SAAAVVLPVLL 548

6 AAAAVLLPVLL 16

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SEQUENCE FROM N.A.

STRAIN=NOD; TISSUE=Thymus;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Xiteunai T., Tashiro H., Itoh M., Aumanoto R., Matsumoto H., Sakaguothi S., Ikegami T., Kashiwagi K., Yamamoto R., Matsumoto H., Sakaguothi S., Ikegami T., Kashiwagi K., Yanamoto R., Ishikawa T., Ozawa Y., Itawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Aokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
 STRAIN=NOD; TISSUE-Thymus; MEDILIBE-20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDILIBE-20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Esperiate I. I. Shibata and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
STRAIN=NOD; TISSUE=Thymus;
REDINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
 Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Rukuda S., Furuno M., Hanagaki T., Hara A., Habhizume W., Hayashida K., Hayatsu W., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 2 days neonet thymus thymic cells cDNA, RIKEN full-
length enriched library, clone:8430018K19 product:matrix
metalloproteinase 14 (membrane-inserted), full insert sequence.
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 STRAIN=NOD; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
582 AA
 Created)
PRT;
 Meth. Enzymol. 303:19-44 (1999).
 (TrEMBLrel. 23, (TrEMBLrel. 23, 1 (TrEMBLrel. 25, 1
 SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
The FANTOM CONSOITIUM,
PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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Gaps

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Length 886; 2; Indels

Score 41; DB 2; Pred. No. 4.4e+02; 4; Mismatches

PRT;

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ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
 886 AA; 98476 MW; 51C734FA9038FF8A CRC64;
 ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKc; 1.
SMART; SM00219; TYRKc; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 513 KKKHKAVLAVAVVPVVI 530
 1 KKKRKA--AAAVLLPVLL 16
 Match 53.9%;
Local Similarity 55.6%;
es 10; Conservative
 PRINTS; PR00019; LEURICHRPT
 Local Similarity 70.6
es 12; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Complete proteome
SEQUENCE 177 AA
 Transferase
 Query Match
 SEQUENCE
 Query Match
 Q7W3J1;
 Q7WEW6
 Q7W3J1
 Matches
 Matches
 RESULT 46
Q7W3J1
 RESULT 47
 Q7WEW6
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 25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Serinc/threonine-specific receptor protein kinase-like.
Name=OSJNBa004H24.55-1; Synonyms=OSJNOa054B01.3-1;
Oryza sativa (faponica cultivar-group).
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Sabaki T., Matsumoto T., Fujisawa M.;
Sabaki T., Matsumoto T., Fujisawa M.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, fosmid
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, fosmid
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, fosmid
submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL, AP007202; BAA470701; -.
GO, GO:000451; F:ATF binding; IEA.
GO; GO:000467; F:protein serime/threonine kinase activity; IEA.
GO; GO:0004472; F:protein serime/threonine kinase activity; IEA.
GO; GO:00044872; F:protein amino acid phosphorylation; IEA.
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (AFR-2002) to the EMBL/GenBank/DDBJ databases.
 ö
 53.9%; Score 41; DB 2; Length 582; 81.8%; Pred. No. 3e+02;
 0; Indels
 Sasaki T., Matsumoto T., Katayose Y.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 PROSITE; PS00546; CYSTEINE SWITCH; 1.
PROSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS01012; ZINC PROFIS, 1.
SEQUENCE 582 AA; 65919 MW; 6CA95CFD5811B093 CRC64;
 MGD; MGI:101900; Mmp14.

MGD; MGI:101900; Mmp14.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

InterPro; IPR001895; Hemopexin.

InterPro; IPR001818; Pept_M10A_M12B.

InterPro; IPR06025; Pept_M10A_M12B.

InterPro; IPR06025; Pept_M Zn_BS.

InterPro; IPR0609709; PGBD_ITke.
 PRT; 886 AA.
 2; Mismatches
 InterPro; IRR07090; LRR plant.
InterPro; IPR007019; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001291; Ser thr pkin AS.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00560; LRR 1; 3.
Pfam; PF00069; Pkinase; 1.
 Pfam; PF00045; Hemopexin; 4.
Pfam; PF0393; Peptidase M10_N; 1.
SMART; PR00138; MATRIXIN.
SMART; SW00120; HX; 4.
SMART; SM00235; ZnMc; 1.
 InterPro; IPR011009; Kinase_like.
InterPro; IPR001611; LRR.
 EMBL; AK088476; BAC40377.1; -.
 Ehrhartoideae; Oryzeae; Oryza
 81.8%;
 9; Conservative
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538 SAAAVVLPVLL 548
 PRELIMINARY;
 6 AAAAVLLPVLL 16
 Best_Local Similarity
Matches 9; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=39947;
 Q6EQK1;
25-OCT-2004 (
25-OCT-2004 (
 Query Match
 Q6EQK1
 RESULT 45
Q6EQK1
 8
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SEQUENCE FROM N.A.

STRAIN=12822 / ATCC BAA-587;

KARDEINEE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINEE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moules S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Numin L., Whitchead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"Nat. Genet. 35:32-4012003."
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 Gaps
 1;
 Bordetella parapertussis.
Bacteria, Proteobacteria; Betaproteobacteria, Burkholderiales;
Alcaligenacese; Bordetella.
NCBI_TaxID=519;
 53.3%; Score 40.5; DB 2; Length 177; 70.6%; Pred. No. 1.2e+02; ive 2; Mismatches 2; Indels 1
 177 AA; 19268 MW; 2A1BDFD4964FFBBB CRC64;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
OrderedLocusNames=BPP4042;
 Last sequence update)
Last annotation update)
 Q'WEW6;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last seq
01-MXR-2004 (TrEMBLrel. 26, Last ann
Hypothetical protein.
 TIGREAMS; TIGR00252; UPF0102; 1.
 EMBL; BX640435; CAE39325.1; -. InterPro; IPR003509; UPF0102. Pfam; PF02021; UPF0102; 1.
 |: | | |||||||||
109 KQGRLARAAALLLPVLL 125
 1 KKKRKA-AAAVLLPVLL 16
 BHHHAD
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162 KKKKAAKILGPILALVALKAALLIPLLL 189
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 Query Match
 FlyBase;
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 SEQUENCE FROM N.A.

STRAIN-RESO / ATCC BAA-588;

When the control of the control
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
R.A. Abril J.F., Asbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
R.A. Abril J.F., Asbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
R.A. Beson K.Y., Benos F.V., Berman B.P., Bhandari D., Boolakov S.,
R.A. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
R.A. Cherry J.W., Cawley S., Dahke C., Davangort L.B., Davies P.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Posler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
R.A. Fosler C., Gabriellan A.E., Garg N.S., Glanar W., Harris M.,
R.A. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 ï
 Gaps
 Ή,
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae; Drosophila.
 53.3%; Score 40.5; DB 2; Length 177; 70.6%; Pred. No. 1.2e+02;
 Indels
 177 AA; 19418 MW; BF6CD86DE3838146 CRC64;
 Last sequence update)
Last annotation update)
 288 AA
 2; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAY-2000 (TrEMBLrel. 13, Last ann
 PRT;
 LIGRFAMS; TIGR00252; UPF0102; 1.
 |: | | |||:||||||
109 KQGRLARAAALLLPVLL 125
 1 KKKRKA-AAAVLLPVLL 16
 Ouery Match
Best Local Similarity 70.0.
Local Similarity 70.0.
Local 21 Conservative
 OrderedLocusNames=BB4515;
 Pfam; PF02021; UPF0102; 1
 PRELIMINARY;
 SEQUENCE FROM N.A.
 Complete proteome
 ORFNames=CG1153;
 NCBI_TaxID=7227;
 NCBI_TaxID=518;
 CG1153-PA.
 SEQUENCE
 Q9VNM7;
 Q9VNM7
 RESULT 48
 MNN 60
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Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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 "Annotation of the Drosophila melanogaster euchromatic genome:
 Score 40.5; DB 2; Length 288; Pred. No. 1.9e+02;
 1; Indels
 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
 EMBL, AE003600; AAF51902.1; -.
FlyBase; FBgn0037414; Osi7.
SEQUENCE 288 AA; 30036 MW; 80F7727D4EE61EA1 CRC64;
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002)
 2; Mismatches
 2 KKRKAA-----AAVLLPVLL 16
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 Conservative
 review.";
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es 12, Conserv
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 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Lewis S.E.;
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 Gaps
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 White spot syndrome virus (WSSV).
Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
VCBI_TaxID=92652;
 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (Fragment).
White spot syndrome virus (WSSV).
Viruses; dsbNA viruses, no RNA stage; Nimaviridae; Whispovirus.
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 Query Match 53.3%; Score 40.5; DB 2; Length 497; Best Local Similarity 66.7%; Pred. No. 3.1e+02; Matches 10; Conservative 2; Mismatches 2; Indels
 [1]
SEQUENCE FROM N.A.
SLOAD X., Hew C.L.;
SUBJANG X., Hew C.L.;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF493145; AAM12816.1; -.
InterPro; IPR00425; MIP.
ROSITE; PS00221; MIP. UNKNOWN 1.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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 318 KRKRNTAAANILLPV 332
 1 KKKRKAAAA-VLLPV 14
 1 KKKRKAAAA-VLLPV 14
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 PRELIMINARY;
 [1]
SEQUENCE FROM N.A. Huang C.
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08029
1D 08029
AC 08029
DT 01-JU
DT 01
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